

SEQUENCE LISTING

<110> Saribas, Sami
Hakes, David
Willet, Scott
Johnson, Karl F.
Bezila, Daniel James
DeFrees, Shawn
Neose Technologies, Inc.

<120> Methods of Refolding Mammalian Glycosyltransferases

<130> 019957-016830PC

<140> WO PCT/US05/03856
<141> 2005-02-04

<150> US 60/542,210
<151> 2004-02-04

<150> US 60/599,406
<151> 2004-08-06

<150> US 60/627,406
<151> 2004-11-12

<160> 80

<170> PatentIn Ver. 2.1

<210> 1
<211> 445
<212> PRT
<213> Homo sapiens

<220>
<223> human beta-1,2-N-acetylglucosaminyltransferase I
(GnTI, GnT1)

<400> 1
Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1 5 10 15
Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro
20 25 30
Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
35 40 45
Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60
Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
65 70 75 80
Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
85 90 95
Val Pro Val Thr Pro Ala Pro Ala Val Ile Pro Ile Leu Val Ile Ala
100 105 110

Cys Asp Arg Ser Thr Val Arg Arg Cys Leu Asp Lys Leu Leu His Tyr
 115 120 125
 Arg Pro Ser Ala Glu Leu Phe Pro Ile Ile Val Ser Gln Asp Cys Gly
 130 135 140
 His Glu Glu Thr Ala Gln Ala Ile Ala Ser Tyr Gly Ser Ala Val Thr
 145 150 155 160
 His Ile Arg Gln Pro Asp Leu Ser Ser Ile Ala Val Pro Pro Asp His
 165 170 175
 Arg Lys Phe Gln Gly Tyr Tyr Lys Ile Ala Arg His Tyr Arg Trp Ala
 180 185 190
 Leu Gly Gln Val Phe Arg Gln Phe Arg Phe Pro Ala Ala Val Val Val
 195 200 205
 Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe Glu Tyr Phe Arg Ala
 210 215 220
 Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu Trp Cys Val Ser Ala
 225 230 235 240
 Trp Asn Asp Asn Gly Lys Glu Gln Met Val Asp Ala Ser Arg Pro Glu
 245 250 255
 Leu Leu Tyr Arg Thr Asp Phe Phe Pro Gly Leu Gly Trp Leu Leu Leu
 260 265 270
 Ala Glu Leu Trp Ala Glu Leu Glu Pro Lys Trp Pro Lys Ala Phe Trp
 275 280 285
 Asp Asp Trp Met Arg Arg Pro Glu Gln Arg Gln Gly Arg Ala Cys Ile
 290 295 300
 Arg Pro Glu Ile Ser Arg Thr Met Thr Phe Gly Arg Lys Gly Val Ser
 305 310 315 320
 His Gly Gln Phe Phe Asp Gln His Leu Lys Phe Ile Lys Leu Asn Gln
 325 330 335
 Gln Phe Val His Phe Thr Gln Leu Asp Leu Ser Tyr Leu Gln Arg Glu
 340 345 350
 Ala Tyr Asp Arg Asp Phe Leu Ala Arg Val Tyr Gly Ala Pro Gln Leu
 355 360 365
 Gln Val Glu Lys Val Arg Thr Asn Asp Arg Lys Glu Leu Gly Glu Val
 370 375 380
 Arg Val Gln Tyr Thr Gly Arg Asp Ser Phe Lys Ala Phe Ala Lys Ala
 385 390 395 400
 Leu Gly Val Met Asp Asp Leu Lys Ser Gly Val Pro Arg Ala Gly Tyr
 405 410 415

Arg Gly Ile Val Thr Phe Gln Phe Arg Gly Arg Arg Val His Leu Ala
420 425 430

Pro Pro Pro Thr Trp Glu Gly Tyr Asp Pro Ser Trp Asn
435 440 445

<210> 2
<211> 447
<212> PRT
<213> Oryctolagus cuniculus

<220>
<223> rabbit beta-1,2-N-acetylglucosaminyltransferase I
(GnTI, GnT1)

<400> 2
Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1 5 10 15

Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro
20 25 30

Val Pro Ser Arg Leu Pro Ser Asp Asn Ala Leu Asp Asp Asp Pro Ala
35 40 45

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50 55 60

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Arg Glu His His Ala
65 70 75 80

Leu Trp Ser Gln Arg Trp Lys Val Pro Thr Ala Ala Pro Pro Ala Gln
85 90 95

Pro His Val Pro Val Thr Pro Pro Ala Val Ile Pro Ile Leu Val
100 105 110

Ile Ala Cys Asp Arg Ser Thr Val Arg Arg Cys Leu Asp Lys Leu Leu
115 120 125

His Tyr Arg Pro Ser Ala Glu Leu Phe Pro Ile Ile Val Ser Gln Asp
130 135 140

Cys Gly His Glu Glu Thr Ala Gln Val Ile Ala Ser Tyr Gly Ser Ala
145 150 155 160

Val Thr His Ile Arg Gln Pro Asp Leu Ser Asn Ile Ala Val Gln Pro
165 170 175

Asp His Arg Lys Phe Gln Gly Tyr Tyr Lys Ile Ala Arg His Tyr Arg
180 185 190

Trp Ala Leu Gly Gln Ile Phe His Asn Phe Asn Tyr Pro Ala Ala Val
195 200 205

Val Val Glu Asp Asp Leu Glu Val Ala Pro Asp Phe Phe Glu Tyr Phe
210 215 220

Gln Ala Thr Tyr Pro Leu Leu Lys Ala Asp Pro Ser Leu Trp Cys Val
225 230 235 240

Ser Ala Trp Asn Asp Asn Gly Lys Glu Gln Met Val Asp Ser Ser Lys
 245 250 255
 Pro Glu Leu Leu Tyr Arg Thr Asp Phe Phe Pro Gly Leu Gly Trp Leu
 260 265 270
 Leu Leu Ala Glu Leu Trp Ala Glu Leu Glu Pro Lys Trp Pro Lys Ala
 275 280 285
 Phe Trp Asp Asp Trp Met Arg Arg Pro Glu Gln Arg Lys Gly Arg Ala
 290 295 300
 Cys Val Arg Pro Glu Ile Ser Arg Thr Met Thr Phe Gly Arg Lys Gly
 305 310 315 320
 Val Ser His Gly Gln Phe Phe Asp Gln His Leu Lys Phe Ile Lys Leu
 325 330 335
 Asn Gln Gln Phe Val Pro Phe Thr Gln Leu Asp Leu Ser Tyr Leu Gln
 340 345 350
 Gln Glu Ala Tyr Asp Arg Asp Phe Leu Ala Arg Val Tyr Gly Ala Pro
 355 360 365
 Gln Leu Gln Val Glu Lys Val Arg Thr Asn Asp Arg Lys Glu Leu Gly
 370 375 380
 Glu Val Arg Val Gln Tyr Thr Gly Arg Asp Ser Phe Lys Ala Phe Ala
 385 390 395 400
 Lys Ala Leu Gly Val Met Asp Asp Leu Lys Ser Gly Val Pro Arg Ala
 405 410 415
 Gly Tyr Arg Gly Ile Val Thr Phe Leu Phe Arg Gly Arg Arg Val His
 420 425 430
 Leu Ala Pro Pro Gln Thr Trp Asp Gly Tyr Asp Pro Ser Trp Thr
 435 440 445

<210> 3
 <211> 342
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Ser mutant

<400> 3
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15
 Arg Ser Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30
 Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95

Phe Arg Phe Pro Ala Ala Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asn Gly Lys Glu
 130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 . 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335

Tyr Asp Pro Ser Trp Asn
 340

<210> 4
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
GnT1) Cys121Ser mutant

<400> 4
gcgggtgattc ccatcctggc catcgctgt gaccgcagca ctgttcggcg ctctctagac 60
aagctgctgc attatcgccc ctccggctgag ctcttccccca tcacatcggttag ccaggactgc 120
gggcacqagg agacggccca ggcacatcgcc tcctacggca ggcgggtcac gcacatccgg 180
cagcccgacc tgagcagcat tgccggctgccc ccggaccacc gcaagttcca gggctactac 240
aagatcgccg gccactaccg ctggggcgctg ggcacgggtct tcggcggatgt tcgcttcccc 300
gcggccgtgg tgggtggagga tgacctggag gtggcccccgg acttcttcga gtactttcg 360
gccacccatcc cgctgctgaa ggcgaccccc tcacatcggt ggcgtctcgcc ctggaaatgac 420
aacggcaagg agcagatggt ggacgcccagc aggccctgagc tgctctaccg caccgacttt 480
ttccctggcc tgggtggct gctgtggcc gagctctggg ctgagctggaa gcccagaatgg 540
ccaaaggccct tctgggacgaa ctggatgcgg cggccggagc agcggcagggg gcgggcctgc 600
atacgccctg agatctcaag aacatgacc ttggccgca agggtgttag ccacgggcag 660
ttctttgacc agcacctcaa gtttatcaag ctgaaccaggc agtttgcata cttcacccag 720
ctggacctgt cttacctgca gcgggaggcc tatgaccgg atttcctcgcc cgcgtctac 780
gggtctcccc agctgcaggt ggagaaatgt aggaccaatg accggaaggaa gctggggag 840
gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
ttccccggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
tgaaattag 1029

<210> 5
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:unpaired
cysteine mutation Cys121Ser mutant region

<400> 5
Ser Thr Val Arg Arg Ser Leu Asp Lys Leu Leu His
1 5 10

<210> 6
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
GnT1) Cys121Asp mutant

<400> 6
Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
1 5 10 15
Arg Asp Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95

Phe Arg Phe Pro Ala Ala Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335

Tyr Asp Pro Ser Trp Asn
 340

<210> 7
 <211> 1029
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Asp mutant

 <400> 7
 gcggtgattc ccatccttgtt catcgctgtt gaccgcagca ctgttcggcg cgatctagac 60
 aagctgctgc attatcggcc ctcggctgag ctcttccccca tcacgtttag ccaggactgc 120
 gggcacgagg agacggccca ggccatcgcc tcctacggca ggcgcgtcac gcacatccgg 180
 cagccccgacc tgagcagcat tgccgtgcg ccggaccacc gcaagttcca gggctactac 240
 aagatcgcgc gccactaccg ctggggcgtg ggccaggtct tccggcagtt tcgcttcccc 300
 gcgccgtgg tgggtggagga tgacctggag gtggcccccgg acttcttca gtaacttccgg 360
 gccacctatc cgctgctgaa ggccgacccc tccctgttgtt gcgtctcgcc ctggaaatgac 420
 aacggcaagg agcagatggt ggacgcccgc aggccctgagc tgctctaccg caccgacttt 480
 ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccaagtgg 540
 ccaaaggccct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcccggctgc 600
 atacgcccctg agatctcaag aacgatgacc tttggccca agggtgttag ccacgggcag 660
 ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgcata cttcacccag 720
 ctggacctgtt ctacactgca gccccggggcc tatgaccggat atttcctcgc ccgcgtctac 780
 ggtgctcccc agctgcaggt ggagaaagtg aggaccaatg accggaagga gctgggggag 840
 gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
 atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
 ttcccggcc gccgtgtcca cctggcgcccc ccaccgacgt gggagggcta tgatccttagc 1020
 tggaattag 1029

<210> 8
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:unpaired
 cysteine mutation Cys121Asp mutant region

<400> 8
 Ser Thr Val Arg Arg Asp Leu Asp Lys Leu Leu His
 1 5 10

<210> 9
 <211> 342
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
 GnT1) Cys121Thr mutant

<400> 9
 Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
 1 5 10 15

 Arg Thr Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
 20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95

Phe Arg Phe Pro Ala Ala Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335

Tyr Asp Pro Ser Trp Asn
 340

<210> 10
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
GnT1) Cys121Thr mutant

<400> 10
gcgggtgattc ccattcctgggt catcgccgtg gaccgcagca ctgttcggcg cactctagac 60
aagctgctgc attatcgccct ctcggctgag ctcttccccca tcatcgtag ccaggactgc 120
gggcacgagg agacggccca ggccatcgcc tcctacggca ggcgggtcac gcacatccgg 180
cagccccgacc tgagcagcat tgccgtgcgc cccggaccacc gcaagttcca gggctactac 240
aagatcgccgc gccactaccg ctggggcgtg ggccaggtct tccggcgtt tcgcttcccc 300
gcggccgtgg tggtgagga tgacctggag gtggcccccgg acttcttca gtaacttcgg 360
gccacccatc cgctgctgaa ggccgacccc tccctgtggt ggcgtctcgcc ctggaatgac 420
aacggcaagg agcagatggt ggacgcccgc aggccctgagc tgctctaccg caccgacttt 480
ttccctggcc tgggctggct gctgttggcc gagctctggg ctgagctgga gcccagaatgg 540
ccaaaggccct tctgggacga ctggatgcgg cggccggagc agcggcaggg gcccggctgc 600
atacggccctg agatctcaag aacgatgacc tttggccgca agggtgtgag ccacgggcag 660
ttctttgacc agcacctcaa gtttatcaag ctgaaccagc agtttgcgttca cttcacccag 720
ctggacctgtt cttaacctgca gccccggaggcc tatgaccggat atttcctcgcc cccgcgtctac 780
ggtgctcccc agctgcaggt ggagaaaatg aggaccaatg accggaagga gctgggggag 840
gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
atggatgacc ttaagtcggg ggttccgaga gctggctacc ggggtattgt caccttccag 960
ttcccgccgccc gccgtgtcca cctggcgcccc ccaccgacgt gggagggcta tgatcctagc 1020
tggaattag 1029

<210> 11
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:unpaired
cysteine mutation Cys121Thr mutant region

<400> 11
Ser Thr Val Arg Arg Thr Leu Asp Lys Leu Leu His
1 5 10

<210> 12
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
GnT1) Cys121Ala mutant

<400> 12
Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
1 5 10 15

Arg Ala Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
20 25 30

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95

Phe Arg Phe Pro Ala Ala Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asp Asn Gly Lys Glu
 130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335

Tyr Asp Pro Ser Trp Asn
 340

```

<210> 13
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
      GnT1) Cys121Ala mutant

<400> 13
gcggtgattc ccatcctggc catcgctgt gaccgcagca ctgttcggcg cgccctagac 60
aagctgctgc attatcgcc ctcggcttag ctcttccca tcacatcgtag ccaggactgc 120
gggcacgagg agacggccca ggccatcgcc tcctacggca ggcgggtcac gcacatccgg 180
cagcccgacc tgagcagcat tgccgtgcgc ccggaccacc gcaagttcca gggctactac 240
aagatcgccg gccactaccg ctggcgctg ggccaggtct tccggcagtt tcgcttcccc 300
gcggccgtgg tggtgagga tgacctggag gtggcccccgg acttcttcga gtactttcgg 360
gccacctata cgctgtgaa ggccgacccc tccctgtggt ggcgtctcgcc ctggaaatgac 420
aacggcaagg agcagatggt ggacgcccagc aggcctgagc tgctctaccg caccgacttt 480
ttccctggcc tgggctggct gctgttgcc gagctctggg ctgagctggg gcccaagtgg 540
ccaaaggcct tctgggacga ctggatgcgg cggccggagc agccggcaggg gcgggcctgc 600
atacggccctg agatctcaag aacatgacc tttggccgca agggtgtgag ccacgggcag 660
ttctttgacc agcacctcaa gtttatcaag ctgaaccaggc agtttgtgca cttcacccag 720
ctggacctgt cttacctgca gcgggaggcc tatgaccgg atttcctcgcc cgcgtctac 780
ggtgctcccc agctgcaggt ggagaaaagtg aggaccaatg accggaaggaa gctggggag 840
gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tgcgcaggc tctgggtgtc 900
atggatgacc ttaagtcggg ggtccgaga gctggctacc ggggtattgt caccttccag 960
ttcccccggcc gccgtgtcca cctggcgccc ccaccgacgt gggaggccta tgatccttagc 1020
tgaaattag                                         1029

<210> 14
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:unpaired
      cysteine mutation Cys121Ala mutant region

<400> 14
Ser Thr Val Arg Arg Ala Leu Asp Lys Leu Leu His
      1           5           10

<210> 15
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
      GnT1) Arg120Ala Cys121His double mutant

<400> 15
Ala Val Ile Pro Ile Leu Val Ile Ala Cys Asp Arg Ser Thr Val Arg
      1           5           10           15

Ala His Leu Asp Lys Leu Leu His Tyr Arg Pro Ser Ala Glu Leu Phe
      20          25          30

```

Pro Ile Ile Val Ser Gln Asp Cys Gly His Glu Glu Thr Ala Gln Ala
 35 40 45

Ile Ala Ser Tyr Gly Ser Ala Val Thr His Ile Arg Gln Pro Asp Leu
 50 55 60

Ser Ser Ile Ala Val Pro Pro Asp His Arg Lys Phe Gln Gly Tyr Tyr
 65 70 75 80

Lys Ile Ala Arg His Tyr Arg Trp Ala Leu Gly Gln Val Phe Arg Gln
 85 90 95

Phe Arg Phe Pro Ala Ala Val Val Glu Asp Asp Leu Glu Val Ala
 100 105 110

Pro Asp Phe Phe Glu Tyr Phe Arg Ala Thr Tyr Pro Leu Leu Lys Ala
 115 120 125

Asp Pro Ser Leu Trp Cys Val Ser Ala Trp Asn Asn Gly Lys Glu
 130 135 140

Gln Met Val Asp Ala Ser Arg Pro Glu Leu Leu Tyr Arg Thr Asp Phe
 145 150 155 160

Phe Pro Gly Leu Gly Trp Leu Leu Leu Ala Glu Leu Trp Ala Glu Leu
 165 170 175

Glu Pro Lys Trp Pro Lys Ala Phe Trp Asp Asp Trp Met Arg Arg Pro
 180 185 190

Glu Gln Arg Gln Gly Arg Ala Cys Ile Arg Pro Glu Ile Ser Arg Thr
 195 200 205

Met Thr Phe Gly Arg Lys Gly Val Ser His Gly Gln Phe Phe Asp Gln
 210 215 220

His Leu Lys Phe Ile Lys Leu Asn Gln Gln Phe Val His Phe Thr Gln
 225 230 235 240

Leu Asp Leu Ser Tyr Leu Gln Arg Glu Ala Tyr Asp Arg Asp Phe Leu
 245 250 255

Ala Arg Val Tyr Gly Ala Pro Gln Leu Gln Val Glu Lys Val Arg Thr
 260 265 270

Asn Asp Arg Lys Glu Leu Gly Glu Val Arg Val Gln Tyr Thr Gly Arg
 275 280 285

Asp Ser Phe Lys Ala Phe Ala Lys Ala Leu Gly Val Met Asp Asp Leu
 290 295 300

Lys Ser Gly Val Pro Arg Ala Gly Tyr Arg Gly Ile Val Thr Phe Gln
 305 310 315 320

Phe Pro Gly Arg Arg Val His Leu Ala Pro Pro Pro Thr Trp Glu Gly
 325 330 335

Tyr Asp Pro Ser Trp Asn
 340

<210> 16
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
beta-1,2-N-acetylglucosaminyltransferase I (GnTI,
GnT1) Arg120Ala Cys121His double mutant

<400> 16
gcgggtgattc ccatcctgggt catcgctgt gaccgcagca ctgttcgggc ccacccatagac 60
aagctgctgc attatcgccct ctcggctgag ctcttcccca tcatacgtag ccaggactgc 120
gggcacgagg agacggccca ggccatcgcc tcctacggca ggcgcggtcac gcacatccgg 180
cagcccgacc tgagcagcat tgccgtgccc ccggaccacc gcaagttcca gggctactac 240
aagatcgccg gccactaccg ctggcgctg ggccaggtct tcggcagtt tcgcttcccc 300
gcggccgtgg tggtgagga tgacctggag gtggcccccgg acttcttcga gtactttcg 360
gccacccatcgccatcgaa ggccgacccc tccctgtggt gcgtctcgcc ctggaaatgac 420
aacggcaagg agcagatggg ggacgcccggc aggcctgagc tgctctaccg caccgacttt 480
ttccctggcc tgggctggct gctgtggcc gagctctggg ctgagctggg gccaagatgg 540
ccaaaggccct tctgggacga ctggatgcgg cgccggagc agccggcaggg gcgggcctgc 600
atacgccctg agatctcaag aacgatgacc tttggccgca agggtgtgag ccacggggcag 660
ttcttgacc agcacctcaa gtttatcaag ctgaaccaggc agtttgtgca cttcacccag 720
ctggacactgt cttacctgca gcgggaggcc tatgaccggc atttcctcgcc cccgcgtctac 780
ggtgctccccc agctgcaggt ggagaaatgg aggaccaatg accggaaggaa gctgggggag 840
gtgcgggtgc agtatacggg cagggacagc ttcaaggctt tcgccaaggc tctgggtgtc 900
atggatgacc ttaagtcggg ggtccgaga gctggctacc ggggtattgt caccttccag 960
ttcccccggcc gccgtgtcca cctggcgccc ccaccgacgt gggagggcta tgatcctagc 1020
tgaaattag 1029

<210> 17
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:unpaired
cysteine mutation Arg120Ala Cys121His double
mutant region

<400> 17
Ser Thr Val Arg Ala His Leu Asp Lys Leu Leu His
1 5 10

<210> 18
<211> 374
<212> PRT
<213> Rattus norvegicus

<220>
<223> rat liver Gal beta-1,3-GalNAc
alpha-2,3-sialyltransferase III (ST3GalIII)

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> delta28 deletion

<400> 18

Met Gly Leu Leu Val Phe Val Arg Asn Leu Leu Leu Ala Leu Cys Leu
1 5 10 15

Phe Leu Val Leu Gly Phe Leu Tyr Tyr Ser Ala Trp Lys Leu His Leu
20 25 30

Leu Gln Trp Glu Asp Ser Asn Ser Leu Ile Leu Ser Leu Asp Ser Ala
35 40 45

Gly Gln Thr Leu Gly Thr Glu Tyr Asp Arg Leu Gly Phe Leu Leu Lys
50 55 60

Leu Asp Ser Lys Leu Pro Ala Glu Leu Ala Thr Lys Tyr Ala Asn Phe
65 70 75 80

Ser Glu Gly Ala Cys Lys Pro Gly Tyr Ala Ser Ala Met Met Thr Ala
85 90 95

Ile Phe Pro Arg Phe Ser Lys Pro Ala Pro Met Phe Leu Asp Asp Ser
100 105 110

Phe Arg Lys Trp Ala Arg Ile Arg Glu Phe Val Pro Pro Phe Gly Ile
115 120 125

Lys Gly Gln Asp Asn Leu Ile Lys Ala Ile Leu Ser Val Thr Lys Glu
130 135 140

Tyr Arg Leu Thr Pro Ala Leu Asp Ser Leu His Cys Arg Arg Cys Ile
145 150 155 160

Ile Val Gly Asn Gly Val Leu Ala Asn Lys Ser Leu Gly Ser Arg
165 170 175

Ile Asp Asp Tyr Asp Ile Val Ile Arg Leu Asn Ser Ala Pro Val Lys
180 185 190

Gly Phe Glu Lys Asp Val Gly Ser Lys Thr Thr Leu Arg Ile Thr Tyr
195 200 205

Pro Glu Gly Ala Met Gln Arg Pro Glu Gln Tyr Glu Arg Asp Ser Leu
210 215 220

Phe Val Leu Ala Gly Phe Lys Trp Gln Asp Phe Lys Trp Leu Lys Tyr
225 230 235 240

Ile Val Tyr Lys Glu Arg Val Ser Ala Ser Asp Gly Phe Trp Lys Ser
245 250 255

Val Ala Thr Arg Val Pro Lys Glu Pro Pro Glu Ile Arg Ile Leu Asn
260 265 270

Pro Tyr Phe Ile Gln Glu Ala Ala Phe Thr Leu Ile Gly Leu Pro Phe
275 280 285

Asn Asn Gly Leu Met Gly Arg Gly Asn Ile Pro Thr Leu Gly Ser Val
290 295 300

Ala Val Thr Met Ala Leu Asp Gly Cys Asp Glu Val Ala Val Ala Gly
305 310 315 320

Phe Gly Tyr Asp Met Asn Thr Pro Asn Ala Pro Leu His Tyr Tyr Glu
325 330 335

Thr Val Arg Met Ala Ala Ile Lys Glu Ser Trp Thr His Asn Ile Gln
340 345 350

Arg Glu Lys Glu Phe Leu Arg Lys Leu Val Lys Ala Arg Val Ile Thr
355 360 365

Asp Leu Ser Ser Gly Ile
370

<210> 19

<211> 555

<212> PRT

<213> Homo sapiens

<220>

<223> human full-length
UDP-N-acetylgalactosaminyltransferase 2 (GalNAcT2)

<400> 19

Met Arg Arg Arg Ser Arg Met Leu Leu Cys Phe Ala Phe Leu Trp Val
1 5 10 15

Leu Gly Ile Ala Tyr Tyr Met Tyr Ser Gly Gly Ser Ala Leu Ala
20 25 30

Gly Gly Ala Gly Gly Ala Gly Arg Lys Glu Asp Trp Asn Glu Ile
35 40 45

Asp Pro Ile Lys Lys Asp Leu His His Ser Asn Gly Glu Glu Lys
50 55 60

Ala Gln Ser Met Glu Thr Leu Pro Pro Gly Lys Val Arg Trp Pro Asp
65 70 75 80

Phe Asn Gln Glu Ala Tyr Val Gly Gly Thr Met Val Arg Ser Gly Gln
85 90 95

Asp Pro Tyr Ala Arg Asn Lys Phe Asn Gln Val Glu Ser Asp Lys Leu
100 105 110

Arg Met Asp Arg Ala Ile Pro Asp Thr Arg His Asp Gln Cys Gln Arg
115 120 125

Lys Gln Trp Arg Val Asp Leu Pro Ala Thr Ser Val Val Ile Thr Phe
130 135 140

His Asn Glu Ala Arg Ser Ala Leu Leu Arg Thr Val Val Ser Val Leu
145 150 155 160

Lys Lys Ser Pro Pro His Leu Ile Lys Glu Ile Ile Leu Val Asp Asp
165 170 175

Tyr Ser Asn Asp Pro Glu Asp Gly Ala Leu Leu Gly Lys Ile Glu Lys
180 185 190

Val Arg Val Leu Arg Asn Asp Arg Arg Glu Gly Leu Met Arg Ser Arg
195 200 205

Val Arg Gly Ala Asp Ala Ala Gln Ala Lys Val Leu Thr Phe Leu Asp
 210 215 220
 Ser His Cys Glu Cys Asn Glu His Trp Leu Glu Pro Leu Leu Glu Arg
 225 230 235 240
 Val Ala Glu Asp Arg Thr Arg Val Val Ser Pro Ile Ile Asp Val Ile
 245 250 255
 Asn Met Asp Asn Phe Gln Tyr Val Gly Ala Ser Ala Asp Leu Lys Gly
 260 265 270
 Gly Phe Asp Trp Asn Leu Val Phe Lys Trp Asp Tyr Met Thr Pro Glu
 275 280 285
 Gln Arg Arg Ser Arg Gln Gly Asn Pro Val Ala Pro Ile Lys Thr Pro
 290 295 300
 Met Ile Ala Gly Gly Leu Phe Val Met Asp Lys Phe Tyr Phe Glu Glu
 305 310 315 320
 Leu Gly Lys Tyr Asp Met Met Asp Val Trp Gly Gly Glu Asn Leu
 325 330 335
 Glu Ile Ser Phe Arg Val Trp Gln Cys Gly Gly Ser Leu Glu Ile Ile
 340 345 350
 Pro Cys Ser Arg Val Gly His Val Phe Arg Lys Gln His Pro Tyr Thr
 355 360 365
 Phe Pro Gly Gly Ser Gly Thr Val Phe Ala Arg Asn Thr Arg Arg Ala
 370 375 380
 Ala Glu Val Trp Met Asp Glu Tyr Lys Asn Phe Tyr Tyr Ala Ala Val
 385 390 395 400
 Pro Ser Ala Arg Asn Val Pro Tyr Gly Asn Ile Gln Ser Arg Leu Glu
 405 410 415
 Leu Arg Lys Lys Leu Ser Cys Lys Pro Phe Lys Trp Tyr Leu Glu Asn
 420 425 430
 Val Tyr Pro Glu Leu Arg Val Pro Asp His Gln Asp Ile Ala Phe Gly
 435 440 445
 Ala Leu Gln Gln Gly Thr Asn Cys Leu Asp Thr Leu Gly His Phe Ala
 450 455 460
 Asp Gly Val Val Gly Val Tyr Glu Cys His Asn Ala Gly Gly Asn Gln
 465 470 475 480
 Glu Trp Ala Leu Thr Lys Glu Lys Ser Val Lys His Met Asp Leu Cys
 485 490 495
 Cys Arg Glu Asn Asp Ser Arg Gln Lys Trp Glu Gln Ile Glu Gly Asn
 500 505 510
 Ser Lys Leu Arg His Val Gly Ser Asn Leu Cys Leu Asp Ser Arg Thr
 515 520 525

Ala Lys Ser Gly Gly Leu Ser Val Glu Val Cys Gly Pro Ala Leu Ser
530 535 540

Gln Gln Trp Lys Phe Thr Leu Asn Leu Gln Gln
545 550 555

<210> 20
<211> 1713
<212> DNA
<213> Homo sapiens

<220>
<223> human full-length
UDP-N-acetylgalactosaminyltransferase 2 (GalNAcT2)

<400> 20
atgcggcggc gctcgccggat gctgctctgc ttgccttcc tgggggtgct gggcatcgcc 60
tactacatgt actcgggggg cggtctcgcg ctggccgggg gcgcggggcg cggtcgccggc 120
aggaaggagg actggaatga aattgacccc attaaaaaga aagaccttca tcacagcaat 180
ggagaagaga aagcacaaag catggagacc ctccctccag gaaagatcg gtggccagac 240
tttaaccagg aagttatgt tgaggggacg atggccgtc cggggcagga cccttacgcc 300
cgcaacaagt tcaaccagggt ggagagtat aagttcgaa tggacagagc catccctgac 360
acccggcatg accagtgtca gggaaagcag tggcggtgg atctgcccgc caccagcgtg 420
gtgatcacgt ttcacaatga agccaggtcg gcccctactca gacccgtgt cagcgtgctt 480
aagaaaagcc cgccccatct cataaaagaa atcatcttgg tggatgacta cagaatgat 540
cctgaggacg gggctctt gggaaaatt gagaaggatc gagttcttag aaatgatcga 600
cgagaaggcc tcatgcgtc acgggttcgg gggccgatg ctgcccgaac caaggtcctg 660
accttcctgg acagtcaactg cgagtgtat gggacttgc tggagccctt cctggaaagg 720
gtggcggagg acaggactcg gttgtgtca cccatcatcg atgtcattaa tatggacaac 780
tttcagtatg tggggcattc tgcgtactt aaggccgtt ttgattggaa cttgttattc 840
aagtgggatt acatgacgcc tgacagaga aggtcccggc aggggaaccc agtcgcccct 900
ataaaaaccc ccatgatttc tggatggctt tttgtatgg ataagttcta ttttgaagaa 960
ctggggaaagt acgacatgtat gatggatgtg tggggaggag agaacataga gatctcggtc 1020
cgctgtgtggc agtgtgtgg cggcttggag atcatccgtt gcaaggctgtt gggacacgtg 1080
ttccggaaaggc agcaccctca cacttcccg ggtggcgtt gcaactgtt tgcccgaaac 1140
acccggccggg cagcagaggt ctggatggat gaataaaaaa atttctattt tgcaagcgtg 1200
ccttctgtca gaaacgttcc ttatggaaat attcagagca gattggaggt taggaagaaa 1260
ctcagctgca agccttcaa atggtaacctt gaaaatgtctt atccagaggtt aagggttcca 1320
gaccatcagg atatagtttt tggggcattt cagcaggaa ctaactgcctt cgacactttg 1380
ggacactttt ctgtatgggtt gtttgaggtt tatgaatgtc acaatgtgg gggaaaccag 1440
gaatgggcct tgacgaagga gaagtccgtt aagcacatgg atttgtgcct tactgtgggt 1500
gaccgggcac cgggctcttct tataaagctg cagggtgtcc gagaaaatga cagcagacag 1560
aaatgggaac agatcgaggg caactccaaatg ctgaggcactg tggcagcaa cctgtgcctg 1620
gacagtgcga cggccaagag cggggcccta agcgtggagg tttgtggccc gccccttcg 1680
cagcagtggaa agttcacgtt caacatcgat cag 1713

<210> 21
<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:delta51
UDP-N-acetylgalactosaminyltransferase 2
(delta51GalNAcT2)

<400> 21
Lys Lys Lys Asp Leu His His Ser Asn Gly Glu Glu Lys Ala Gln Ser
1 5 10 15

Met	Glu	Thr	Leu	Pro	Pro	Gly	Lys	Val	Arg	Trp	Pro	Asp	Phe	Asn	Gln
20								25						30	
Glu	Ala	Tyr	Val	Gly	Gly	Thr	Met	Val	Arg	Ser	Gly	Gln	Asp	Pro	Tyr
35								40						45	
Ala	Arg	Asn	Lys	Phe	Asn	Gln	Val	Glu	Ser	Asp	Lys	Leu	Arg	Met	Asp
50							55				60				
Arg	Ala	Ile	Pro	Asp	Thr	Arg	His	Asp	Gln	Cys	Gln	Arg	Lys	Gln	Trp
65							70			75			80		
Arg	Val	Asp	Leu	Pro	Ala	Thr	Ser	Val	Val	Ile	Thr	Phe	His	Asn	Glu
85								90						95	
Ala	Arg	Ser	Ala	Leu	Leu	Arg	Thr	Val	Val	Ser	Val	Leu	Lys	Lys	Ser
100								105						110	
Pro	Pro	His	Leu	Ile	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Tyr	Ser	Asn
115							120						125		
Asp	Pro	Glu	Asp	Gly	Ala	Leu	Leu	Gly	Lys	Ile	Glu	Lys	Val	Arg	Val
130							135				140				
Leu	Arg	Asn	Asp	Arg	Arg	Glu	Gly	Leu	Met	Arg	Ser	Arg	Val	Arg	Gly
145							150			155			160		
Ala	Asp	Ala	Ala	Gln	Ala	Lys	Val	Leu	Thr	Phe	Leu	Asp	Ser	His	Cys
165								170						175	
Glu	Cys	Asn	Glu	His	Trp	Leu	Glu	Pro	Leu	Leu	Glu	Arg	Val	Ala	Glu
180							185				190				
Asp	Arg	Thr	Arg	Val	Val	Ser	Pro	Ile	Ile	Asp	Val	Ile	Asn	Met	Asp
195							200				205				
Asn	Phe	Gln	Tyr	Val	Gly	Ala	Ser	Ala	Asp	Leu	Lys	Gly	Gly	Phe	Asp
210							215				220				
Trp	Asn	Leu	Val	Phe	Lys	Trp	Asp	Tyr	Met	Thr	Pro	Glu	Gln	Arg	Arg
225							230			235			240		
Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro	Met	Ile	Ala
245								250						255	
Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu	Leu	Gly	Lys
260							265				270				
Tyr	Asp	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu	Glu	Ile	Ser	
275							280				285				
Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile	Pro	Cys	Ser
290							295				300				
Arg	Val	Gly	His	Val	Phe	Arg	Lys	Gln	His	Pro	Tyr	Thr	Phe	Pro	Gly
305							310				315			320	
Gly	Ser	Gly	Thr	Val	Phe	Ala	Arg	Asn	Thr	Arg	Arg	Ala	Ala	Glu	Val
325								330						335	

Trp Met Asp Glu Tyr Lys Asn Phe Tyr Tyr Ala Ala Val Pro Ser Ala
 340 345 350
 Arg Asn Val Pro Tyr Gly Asn Ile Gln Ser Arg Leu Glu Leu Arg Lys
 355 360 365
 Lys Leu Ser Cys Lys Pro Phe Lys Trp Tyr Leu Glu Asn Val Tyr Pro
 370 375 380
 Glu Leu Arg Val Pro Asp His Gln Asp Ile Ala Phe Gly Ala Leu Gln
 385 390 395 400
 Gln Gly Thr Asn Cys Leu Asp Thr Leu Gly His Phe Ala Asp Gly Val
 405 410 415
 Val Gly Val Tyr Glu Cys His Asn Ala Gly Gly Asn Gln Glu Trp Ala
 420 425 430
 Leu Thr Lys Glu Lys Ser Val Lys His Met Asp Leu Cys Leu Thr Val
 435 440 445
 Val Asp Arg Ala Pro Gly Ser Leu Ile Lys Leu Gln Gly Cys Arg Glu
 450 455 460
 Asn Asp Ser Arg Gln Lys Trp Glu Gln Ile Glu Gly Asn Ser Lys Leu
 465 470 475 480
 Arg His Val Gly Ser Asn Leu Cys Leu Asp Ser Arg Thr Ala Lys Ser
 485 490 495
 Gly Gly Leu Ser Val Glu Val Cys Gly Pro Ala Leu Ser Gln Gln Trp
 500 505 510
 Lys Phe Thr Leu Asn Leu Gln Gln
 515 520

<210> 22
 <211> 1560
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:delta51
 UDP-N-acetylgalactosaminyltransferase 2
 (delta51GalNAcT2)

<400> 22
 aaaaagaaaag actttcatca cagcaatgga gaagagaaaag cacaaggcat ggagaccctc 60
 cttccaggga aagtacggtg gccagactt aaccaggaag cttatgttgg agggacgatg 120
 gtccgctccg ggcaggaccc ttacgcccgc aacaagttca accaggtgga gagtgataag 180
 cttcgaatgg acagagccat ccctgacacc cggcatgacc agtgtcagcg gaagcagtgg 240
 cgggtggatc tgccggccac cagcgtggtg atcacgttcc acaatgaagc caggtcggcc 300
 ctactcagga ccgtggtcag cgtgcttaag aaaaggccgc cccatctcat aaaagaaaatc 360
 atcttggtgg atgactacag caatgatcct gaggacgggg ctctcttggg gaaaattgag 420
 aaagtgcgag ttcttagaaa tcatcgacga gaaggcctca tgcgctcacg gtttcgggg 480
 gccgatgctg cccaaagccaa ggtcctgacc ttcctggaca gtcactgcga gtgtaatgag 540
 cactggctgg agcccctcct gggaaagggtg gcggaggaca ggactcgggt tgggtcaccc 600
 atcatcgatg tcattaaat ggcacaactt cagttatgtgg gggcatctgc tgacttgaag 660
 ggcggtttg attggaactt ggtattcaag tgggattaca tgacgcctga gcagagaagg 720
 tccccggcagg ggaacccagt cggccctata aaaaccccca tgattgtctg tgggtcttt 780

gtgatggata agttctatgg tgaagaactgggaaagtacg acatgatgatggatgtgtgg 840
ggaggagaga acctagagat ctcgttccgcgtgtggcagt gtgggtggcagcctggagatc 900
atcccggtca gccgtgtggg acacgtgttc cggaaagcagc acccctacac gttcccggt 960
ggcagtggca ctgtcttgc ccgaaacacc cggcggcagcagaggtctg gatggatgaa 1020
tacaaaaatt tctattatgc agcagtgcct tctgctagaa acgttcctta tggaaatatt 1080
cagagcagat tggagcttag gaagaaaactc agctgcaagc ctttcaaattgtacccctgaa 1140
aatgtctatc cagagttaaagggttccagac catcaggata tagctttgg ggccttgcag 1200
cagggaaacta actgcctcga cactttgggactcttgcgtatgggtgggttggagttat 1260
gaatgtcaca atgctggggaaaccaggaa tggccttga cgaaggagaa gtcgggtgaag 1320
cacatggatt tgccttac tgggtggac cgggcaccgg gctctttat aaagctgcag 1380
ggctgcccggag aaaatgacagcagacagaaatggaaacaga tggaggcgttgccttgc 1440
aggcacgtgg gcagcaaccttgccttgcactgcacgg ccaagagcgg gggcctaagc 1500
gtggaggtgttggcccttcgcagcagtggaaatgttgcacgttgc 1560

<210> 23
<211> 691
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:maltose binding
protein-Gal beta-1,3-GalNAc
alpha-2,3-sialyltransferase 1 (MBP-ST3Gal1) fusion
protein

<400> 23
Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380
 Glu Gly Arg Ile Ser Glu Phe Gly Ser Glu Leu Ser Glu Asn Phe Lys
 385 390 395 400
 Lys Leu Met Lys Tyr Pro Tyr Arg Pro Cys Thr Cys Thr Arg Cys Ile
 405 410 415
 Glu Glu Gln Arg Val Ser Ala Trp Phe Asp Glu Arg Phe Asn Arg Ser
 420 425 430
 Met Gln Pro Leu Leu Thr Ala Lys Asn Ala His Leu Glu Glu Asp Thr
 435 440 445
 Tyr Lys Trp Trp Leu Arg Leu Gln Arg Glu Lys Gln Pro Asn Asn Leu
 450 455 460
 Asn Asp Thr Ile Arg Glu Leu Phe Gln Val Val Pro Gly Asn Val Asp
 465 470 475 480
 Pro Leu Leu Glu Lys Arg Leu Val Ser Cys Arg Arg Cys Ala Val Val
 485 490 495

Gly Asn Ser Gly Asn Leu Lys Glu Ser Tyr Tyr Gly Pro Gln Ile Asp
 500 505 510
 Ser His Asp Phe Val Leu Arg Met Asn Lys Ala Pro Thr Glu Gly Phe
 515 520 525
 Glu Ala Asp Val Gly Ser Lys Thr Thr His His Phe Val Tyr Pro Glu
 530 535 540
 Ser Phe Arg Glu Leu Ala Gln Glu Val Ser Met Ile Leu Val Pro Phe
 545 550 555 560
 Lys Thr Thr Asp Leu Glu Trp Val Ile Ser Ala Thr Thr Thr Gly Arg
 565 570 575
 Ile Ser His Thr Tyr Val Pro Val Pro Ala Lys Ile Lys Val Lys Lys
 580 585 590
 Glu Lys Ile Leu Ile Tyr His Pro Ala Phe Ile Lys Tyr Val Phe Asp
 595 600 605
 Arg Trp Leu Gln Gly His Gly Arg Tyr Pro Ser Thr Gly Ile Leu Ser
 610 615 620
 Val Ile Phe Ser Leu His Ile Cys Asp Glu Val Asp Leu Tyr Gly Phe
 625 630 635 640
 Gly Ala Asp Ser Lys Gly Asn Trp His His Tyr Trp Glu Asn Asn Pro
 645 650 655
 Ser Ala Gly Ala Phe Arg Lys Thr Gly Val His Asp Gly Asp Phe Glu
 660 665 670
 Ser Asn Val Thr Thr Ile Leu Ala Ser Ile Asn Lys Ile Arg Ile Phe
 675 680 685
 Lys Gly Arg
 690

<210> 24
 <211> 841
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-starch binding domain-Gal beta-1,3-GalNAc
 alpha-2,3-sialyltransferase 1 (MBP-SBD-ST3Gal1)
 fusion protein

<400> 24
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365

Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380
 Glu Gly Arg Ile Ser Glu Phe Gly Ser Ile Val Ala Thr Gly Gly Thr
 385 390 395 400
 Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser Thr Ser
 405 410 415
 Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser Thr
 420 425 430
 Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala
 435 440 445
 Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln
 450 455 460
 Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys
 465 470 475 480
 Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala
 485 490 495
 Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser
 500 505 510
 Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala
 515 520 525
 Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg Gly Ser Glu
 530 535 540
 Leu Ser Glu Asn Phe Lys Lys Leu Met Lys Tyr Pro Tyr Arg Pro Cys
 545 550 555 560
 Thr Cys Thr Arg Cys Ile Glu Glu Gln Arg Val Ser Ala Trp Phe Asp
 565 570 575
 Glu Arg Phe Asn Arg Ser Met Gln Pro Leu Leu Thr Ala Lys Asn Ala
 580 585 590
 His Leu Glu Glu Asp Thr Tyr Lys Trp Trp Leu Arg Leu Gln Arg Glu
 595 600 605
 Lys Gln Pro Asn Asn Leu Asn Asp Thr Ile Arg Glu Leu Phe Gln Val
 610 615 620
 Val Pro Gly Asn Val Asp Pro Leu Leu Glu Lys Arg Leu Val Ser Cys
 625 630 635 640
 Arg Arg Cys Ala Val Val Gly Asn Ser Gly Asn Leu Lys Glu Ser Tyr
 645 650 655
 Tyr Gly Pro Gln Ile Asp Ser His Asp Phe Val Leu Arg Met Asn Lys
 660 665 670
 Ala Pro Thr Glu Gly Phe Glu Ala Asp Val Gly Ser Lys Thr Thr His
 675 680 685

His	Phe	Val	Tyr	Pro	Glu	Ser	Phe	Arg	Glu	Leu	Ala	Gln	Glu	Val	Ser
690					695					700					
Met	Ile	Leu	Val	Pro	Phe	Lys	Thr	Thr	Asp	Leu	Glu	Trp	Val	Ile	Ser
705					710					715			720		
Ala	Thr	Thr	Thr	Gly	Arg	Ile	Ser	His	Thr	Tyr	Val	Pro	Val	Pro	Ala
	725						730						735		
Lys	Ile	Lys	Val	Lys	Lys	Glu	Ile	Leu	Ile	Tyr	His	Pro	Ala	Phe	
	740					745					750				
Ile	Lys	Tyr	Val	Phe	Asp	Arg	Trp	Leu	Gln	Gly	His	Gly	Arg	Tyr	Pro
	755					760					765				
Ser	Thr	Gly	Ile	Leu	Ser	Val	Ile	Phe	Ser	Leu	His	Ile	Cys	Asp	Glu
	770					775					780				
Val	Asp	Leu	Tyr	Gly	Phe	Gly	Ala	Asp	Ser	Lys	Gly	Asn	Trp	His	His
	785					790				795			800		
Tyr	Trp	Glu	Asn	Asn	Pro	Ser	Ala	Gly	Ala	Phe	Arg	Lys	Thr	Gly	Val
						805				810			815		
His	Asp	Gly	Asp	Phe	Glu	Ser	Asn	Val	Thr	Thr	Ile	Leu	Ala	Ser	Ile
	820					825					830				
Asn	Lys	Ile	Arg	Ile	Phe	Lys	Gly	Arg							
	835					840									

<210> 25
 <211> 793
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:maltose binding
 protein-alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I mouse truncation
 fusion protein (MBP-mST6GalNAcI S127)

<220>
 <221> MOD_RES
 <222> (708)
 <223> Xaa = any amino acid

 <400> 25
 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30

 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Lys Phe

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 35 40 45
 50 55 60

His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile
65				70					75				80		
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp
			85					90				95			
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu
	100				105					110					
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys
	115				120						125				
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly
	130				135				140						
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro
	145				150			155			160				
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys
	165				170				175						
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly
	180				185				190						
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp
	195				200				205						
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala
	210				215				220						
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys
	225				230				235			240			
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser
	245				250				255						
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro
	260				265				270						
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp
	275				280				285						
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala
	290				295				300						
Leu	Lys	Ser	Tyr	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	
	305				310				315			320			
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln
	325				330					335					
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala
	340				345				350						
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn
	355				360				365						
Ser	Ser	Ser	Asn	Leu	Gly										
	370				375				380						

Glu Gly Arg Ile Ser Glu Phe Gly Ser Ser Glu His Leu Asp Lys Val
 385 390 395 400
 Pro Arg Thr Pro Gly Ala Leu Ser Thr Arg Lys Thr Pro Met Ala Thr
 405 410 415
 Gly Ala Val Pro Ala Lys Lys Val Val Gln Ala Thr Lys Ser Pro
 420 425 430
 Ala Ser Ser Pro His Pro Thr Thr Arg Arg Arg Gln Arg Leu Lys Ala
 435 440 445
 Ser Glu Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Glu Tyr Ser
 450 455 460
 Leu Asp Met Ser Ser Leu Gln Thr Asn Cys Ser Ala Ser Val Lys Ile
 465 470 475 480
 Lys Ala Ser Lys Ser Pro Trp Leu Gln Asn Ile Phe Leu Pro Asn Ile
 485 490 495
 Thr Leu Phe Leu Asp Ser Gly Arg Phe Thr Gln Ser Glu Trp Asn Arg
 500 505 510
 Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu Asn Gln Ser
 515 520 525
 Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val Arg Gln Gln Gln
 530 535 540
 Leu Leu Leu Ala Ser Leu Pro Thr Gly Tyr Ser Lys Cys Ile Thr Cys
 545 550 555 560
 Ala Val Val Gly Asn Gly Gly Ile Leu Asn Asp Ser Arg Val Gly Arg
 565 570 575
 Glu Ile Asp Ser His Asp Tyr Val Phe Arg Leu Ser Gly Ala Val Ile
 580 585 590
 Lys Gly Tyr Glu Gln Asp Val Gly Thr Arg Thr Ser Phe Tyr Gly Phe
 595 600 605
 Thr Ala Phe Ser Leu Thr Gln Ser Ile Leu Ile Leu Gly Arg Arg Gly
 610 615 620
 Phe Gln His Val Pro Leu Gly Lys Asp Val Arg Tyr Leu His Phe Leu
 625 630 635 640
 Glu Gly Thr Arg Asn Tyr Glu Trp Leu Glu Ala Met Phe Leu Asn Gln
 645 650 655
 Thr Leu Ala Lys Thr His Leu Ser Trp Phe Arg His Arg Pro Gln Glu
 660 665 670
 Ala Phe Arg Asn Ala Leu Asp Leu Asp Arg Tyr Leu Leu His Pro
 675 680 685
 Asp Phe Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu
 690 695 700

Asp	Thr	Ala	Xaa	Trp	Arg	Ile	Tyr	Arg	Pro	Thr	Thr	Gly	Ala	Leu	Leu
705															720
Leu	Leu	Thr	Ala	Leu	His	Leu	Cys	Asp	Lys	Val	Ser	Ala	Tyr	Gly	Phe
															735
Ile	Thr	Glu	Gly	His	Glu	Arg	Phe	Ser	Asp	His	Tyr	Tyr	Asp	Thr	Ser
															750
Trp	Lys	Arg	Leu	Ile	Phe	Tyr	Ile	Asn	His	Asp	Phe	Arg	Leu	Glu	Arg
															765
Met	Val	Trp	Lys	Arg	Leu	His	Asp	Glu	Gly	Ile	Ile	Trp	Leu	Tyr	Gln
															780
Arg	Pro	Gln	Ser	Asp	Lys	Ala	Lys	Asn							
															785
785															

<210> 26
 <211> 958
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:maltose binding
 protein-alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I human truncation
 fusion protein (MBP-hST6GalNAcI K36)

<400> 26																
Met	Lys	Ile	Glu	Glu	Gly	Lys	Leu	Val	Ile	Trp	Ile	Asn	Gly	Asp	Lys	
1															15	
Gly	Tyr	Asn	Gly	Leu	Ala	Glu	Val	Gly	Lys	Lys	Phe	Glu	Lys	Asp	Thr	
															30	
Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	
															45	
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	
															50	
His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
															65	
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	
															85	
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu	
															100	
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys	
															115	
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
															130	
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro	
															145	
145															160	
150															155	

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380
 Glu Gly Arg Ile Ser Glu Phe Gly Ser Lys Glu Pro Gln Thr Lys Pro
 385 390 395 400
 Ser Arg His Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser
 405 410 415
 Leu Ala Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr
 420 425 430
 Ile Tyr Ala Glu Pro Val Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr
 435 440 445
 Gln Pro Lys Ala His Thr Thr Gly Asp Arg Gly Lys Glu Ala Asn Gln
 450 455 460
 Ala Pro Pro Glu Glu Gln Asp Lys Val Pro His Thr Ala Gln Arg Ala
 465 470 475 480

Ala Trp Lys Ser Pro Glu Lys Glu Lys Thr Met Val Asn Thr Leu Ser
 485 490 495
 Pro Arg Gly Gln Asp Ala Gly Met Ala Ser Gly Arg Thr Glu Ala Gln
 500 505 510
 Ser Trp Lys Ser Gln Asp Thr Lys Thr Thr Gln Gly Asn Gly Gly Gln
 515 520 525
 Thr Arg Lys Leu Thr Ala Ser Arg Thr Val Ser Glu Lys His Gln Gly
 530 535 540
 Lys Ala Ala Thr Thr Ala Lys Thr Leu Ile Pro Lys Ser Gln His Arg
 545 550 555 560
 Met Leu Ala Pro Thr Gly Ala Val Ser Thr Arg Thr Arg Gln Lys Gly
 565 570 575
 Val Thr Thr Ala Val Ile Pro Pro Lys Glu Lys Lys Pro Gln Ala Thr
 580 585 590
 Pro Pro Pro Ala Pro Phe Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg
 595 600 605
 Leu Lys Ala Ala Asn Phe Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu
 610 615 620
 Lys Tyr Ser Phe Glu Ile Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser
 625 630 635 640
 Val Lys Ile Lys Ala Ser Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu
 645 650 655
 Pro Asn Leu Thr Leu Phe Leu Asp Ser Arg His Phe Asn Gln Ser Glu
 660 665 670
 Trp Asp Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe Met Glu Leu
 675 680 685
 Asn Tyr Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro Pro Val Pro
 690 695 700
 Gln Gln Gln Leu Leu Ala Ser Leu Pro Ala Gly Ser Leu Arg Cys
 705 710 715 720
 Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn Asn Ser His
 725 730 735
 Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe Arg Leu Ser Gly
 740 745 750
 Ala Leu Ile Lys Gly Tyr Glu Gln Asp Val Gly Thr Arg Thr Ser Phe
 755 760 765
 Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln Ser Leu Leu Ile Leu Gly
 770 775 780
 Asn Arg Gly Phe Lys Asn Val Pro Leu Gly Lys Asp Val Arg Tyr Leu
 785 790 795 800

His Phe Leu Glu Gly Thr Arg Asp Tyr Glu Trp Leu Glu Ala Leu Leu
 805 810 815
 Met Asn Gln Thr Val Met Ser Lys Asn Leu Phe Trp Phe Arg His Arg
 820 825 830
 Pro Gln Glu Ala Phe Arg Glu Ala Leu His Met Asp Arg Tyr Leu Leu
 835 840 845
 Leu His Pro Asp Phe Leu Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser
 850 855 860
 Lys Thr Leu Asp Gly Ala His Trp Arg Ile Tyr Arg Pro Thr Thr Gly
 865 870 875 880
 Ala Leu Leu Leu Leu Thr Ala Leu Gln Leu Cys Asp Gln Val Ser Ala
 885 890 895
 Tyr Gly Phe Ile Thr Glu Gly His Glu Arg Phe Ser Asp His Tyr Tyr
 900 905 910
 Asp Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His Asp Phe Lys
 915 920 925
 Leu Glu Arg Glu Val Trp Lys Arg Leu His Asp Glu Gly Ile Ile Arg
 930 935 940
 Leu Tyr Gln Arg Pro Gly Pro Gly Thr Ala Lys Ala Lys Asn
 945 950 955

<210> 27
 <211> 402
 <212> PRT
 <213> Bos taurus

<220>
 <223> full length bovine beta-1,4-galactosyltransferase
 (GalT1)

<400> 27
 Met Lys Phe Arg Glu Pro Leu Leu Gly Gly Ser Ala Ala Met Pro Gly
 1 5 10 15

Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
 20 25 30

His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Arg
 35 40 45

Arg Leu Pro Gln Leu Val Gly Val His Pro Pro Leu Gln Gly Ser Ser
 50 55 60

His Gly Ala Ala Ala Ile Gly Gln Pro Ser Gly Glu Leu Arg Leu Arg
 65 70 75 80

Gly Val Ala Pro Pro Pro Leu Gln Asn Ser Ser Lys Pro Arg Ser
 85 90 95

Arg Ala Pro Ser Asn Leu Asp Ala Tyr Ser His Pro Gly Pro Gly Pro
 100 105 110

Gly Pro Gly Ser Asn Leu Thr Ser Ala Pro Val Pro Ser Thr Thr Thr
 115 120 125
 Arg Ser Leu Thr Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly Pro
 130 135 140
 Met Leu Ile Glu Phe Asn Ile Pro Val Asp Leu Lys Leu Ile Glu Gln
 145 150 155 160
 Gln Asn Pro Lys Val Lys Leu Gly Gly Arg Tyr Thr Pro Met Asp Cys
 165 170 175
 Ile Ser Pro His Lys Val Ala Ile Ile Leu Phe Arg Asn Arg Gln
 180 185 190
 Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Met Val Gln Arg
 195 200 205
 Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Glu Ser
 210 215 220
 Met Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Phe Lys Glu Ala Leu
 225 230 235 240
 Lys Asp Tyr Asp Tyr Asn Cys Phe Val Phe Ser Asp Val Asp Leu Ile
 245 250 255
 Pro Met Asn Asp His Asn Thr Tyr Arg Cys Phe Ser Gln Pro Arg His
 260 265 270
 Ile Ser Val Ala Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln
 275 280 285
 Tyr Phe Gly Gly Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Ser Ile
 290 295 300
 Asn Gly Phe Pro Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp
 305 310 315 320
 Ile Tyr Asn Arg Leu Ala Phe Arg Gly Met Ser Val Ser Arg Pro Asn
 325 330 335
 Ala Val Ile Gly Lys Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys
 340 345 350
 Asn Glu Pro Asn Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu
 355 360 365
 Thr Met Leu Ser Asp Gly Leu Asn Ser Leu Thr Tyr Met Val Leu Glu
 370 375 380
 Val Gln Arg Tyr Pro Leu Tyr Thr Lys Ile Thr Val Asp Ile Gly Thr
 385 390 395 400
 Pro Ser

<210> 28
 <211> 343
 <212> PRT
 <213> Sus scrofa

<220>

<223> full length porcine Gal beta-1,3-GalNAc
alpha-2,3-sialyltransferase 1 (ST3Gal1)

<400> 28

Met Ala Pro Met Arg Lys Lys Ser Thr Leu Lys Leu Leu Thr Leu Leu
1 5 10 15

Val Leu Phe Ile Phe Leu Thr Ser Phe Phe Leu Asn Tyr Ser His Thr
20 25 30

Val Val Thr Thr Ala Trp Phe Pro Lys Gln Met Val Ile Glu Leu Ser
35 40 45

Glu Asn Phe Lys Lys Leu Met Lys Tyr Pro Tyr Arg Pro Cys Thr Cys
50 55 60

Thr Arg Cys Ile Glu Glu Gln Arg Val Ser Ala Trp Phe Asp Glu Arg
65 70 75 80

Phe Asn Arg Ser Met Gln Pro Leu Leu Thr Ala Lys Asn Ala His Leu
85 90 95

Glu Glu Asp Thr Tyr Lys Trp Trp Leu Arg Leu Gln Arg Glu Lys Gln
100 105 110

Pro Asn Asn Leu Asn Asp Thr Ile Arg Glu Leu Phe Gln Val Val Pro
115 120 125

Gly Asn Val Asp Pro Leu Leu Glu Lys Arg Leu Val Ser Cys Arg Arg
130 135 140

Cys Ala Val Val Gly Asn Ser Gly Asn Leu Lys Glu Ser Tyr Tyr Gly
145 150 155 160

Pro Gln Ile Asp Ser His Asp Phe Val Leu Arg Met Asn Lys Ala Pro
165 170 175

Thr Glu Gly Phe Glu Ala Asp Val Gly Ser Lys Thr Thr His His Phe
180 185 190

Val Tyr Pro Glu Ser Phe Arg Glu Leu Ala Gln Glu Val Ser Met Ile
195 200 205

Leu Val Pro Phe Lys Thr Thr Asp Leu Glu Trp Val Ile Ser Ala Thr
210 215 220

Thr Thr Gly Thr Ile Ser His Thr Tyr Val Pro Val Pro Ala Lys Ile
225 230 235 240

Lys Val Lys Lys Glu Lys Ile Leu Ile Tyr His Pro Ala Phe Ile Lys
245 250 255

Tyr Val Phe Asp Arg Trp Leu Gln Gly His Gly Arg Tyr Pro Ser Thr
260 265 270

Gly Ile Leu Ser Val Ile Phe Ser Leu His Ile Cys Asp Glu Val Asp
275 280 285

Leu Tyr Gly Phe Gly Ala Asp Ser Lys Gly Asn Trp His His Tyr Trp
290 295 300

Glu Asn Asn Pro Ser Ala Gly Ala Phe Arg Lys Thr Gly Val His Asp
305 310 315 320

Gly Asp Phe Glu Ser Asn Val Thr Thr Ile Leu Ala Ser Ile Asn Lys
325 330 335

Ile Arg Ile Phe Lys Gly Arg
340

<210> 29

<211> 600

<212> PRT

<213> Homo sapiens

<220>

<223> human alpha-N-acetylgalactosaminide
alpha-2,6-sialyltransferase I (ST6GalNAcTI)

<400> 29

Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val Gln
1 5 10 15

Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala Leu Pro
20 25 30

Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His Gln Arg Thr
35 40 45

Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala Lys Pro Lys Ser
50 55 60

Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile Tyr Ala Glu Pro Val
65 70 75 80

Pro Glu Asn Asn Ala Leu Asn Thr Gln Thr Gln Pro Lys Ala His Thr
85 90 95

Thr Gly Asp Arg Gly Lys Glu Ala Asn Gln Ala Pro Pro Glu Glu Gln
100 105 110

Asp Lys Val Pro His Thr Ala Gln Arg Ala Ala Trp Lys Ser Pro Glu
115 120 125

Lys Glu Lys Thr Met Val Asn Thr Leu Ser Pro Arg Gly Gln Asp Ala
130 135 140

Gly Met Ala Ser Gly Arg Thr Glu Ala Gln Ser Trp Lys Ser Gln Asp
145 150 155 160

Thr Lys Thr Thr Gln Gly Asn Gly Gln Thr Arg Lys Leu Thr Ala
165 170 175

Ser Arg Thr Val Ser Glu Lys His Gln Gly Lys Ala Ala Thr Thr Ala
180 185 190

Lys Thr Leu Ile Pro Lys Ser Gln His Arg Met Leu Ala Pro Thr Gly
195 200 205

Ala Val Ser Thr Arg Thr Arg Gln Lys Gly Val Thr Thr Ala Val Ile
210 215 220

Pro Pro Lys Glu Lys Lys Pro Gln Ala Thr Pro Pro Pro Ala Pro Phe
 225 230 235 240
 Gln Ser Pro Thr Thr Gln Arg Asn Gln Arg Leu Lys Ala Ala Asn Phe
 245 250 255
 Lys Ser Glu Pro Arg Trp Asp Phe Glu Glu Lys Tyr Ser Phe Glu Ile
 260 265 270
 Gly Gly Leu Gln Thr Thr Cys Pro Asp Ser Val Lys Ile Lys Ala Ser
 275 280 285
 Lys Ser Leu Trp Leu Gln Lys Leu Phe Leu Pro Asn Leu Thr Leu Phe
 290 295 300
 Leu Asp Ser Arg His Phe Asn Gln Ser Glu Trp Asp Arg Leu Glu His
 305 310 315 320
 Phe Ala Pro Pro Phe Gly Phe Met Glu Leu Asn Tyr Ser Leu Val Gln
 325 330 335
 Lys Val Val Thr Arg Phe Pro Pro Val Pro Gln Gln Gln Leu Leu Leu
 340 345 350
 Ala Ser Leu Pro Ala Gly Ser Leu Arg Cys Ile Thr Cys Ala Val Val
 355 360 365
 Gly Asn Gly Gly Ile Leu Asn Asn Ser His Met Gly Gln Glu Ile Asp
 370 375 380
 Ser His Asp Tyr Val Phe Arg Leu Ser Gly Ala Leu Ile Lys Gly Tyr
 385 390 395 400
 Glu Gln Asp Val Gly Thr Arg Thr Ser Phe Tyr Gly Phe Thr Ala Phe
 405 410 415
 Ser Leu Thr Gln Ser Leu Leu Ile Leu Gly Asn Arg Gly Phe Lys Asn
 420 425 430
 Val Pro Leu Gly Lys Asp Val Arg Tyr Leu His Phe Leu Glu Gly Thr
 435 440 445
 Arg Asp Tyr Glu Trp Leu Glu Ala Leu Leu Met Asn Gln Thr Val Met
 450 455 460
 Ser Lys Asn Leu Phe Trp Phe Arg His Arg Pro Gln Glu Ala Phe Arg
 465 470 475 480
 Glu Ala Leu His Met Asp Arg Tyr Leu Leu Leu His Pro Asp Phe Leu
 485 490 495
 Arg Tyr Met Lys Asn Arg Phe Leu Arg Ser Lys Thr Leu Asp Gly Ala
 500 505 510
 His Trp Arg Ile Tyr Arg Pro Thr Thr Gly Ala Leu Leu Leu Thr
 515 520 525
 Ala Leu Gln Leu Cys Asp Gln Val Ser Ala Tyr Gly Phe Ile Thr Glu
 530 535 540

Gly His Glu Arg Phe Ser Asp His Tyr Tyr Asp Thr Ser Trp Lys Arg
 545 550 555 560

Leu Ile Phe Tyr Ile Asn His Asp Phe Lys Leu Glu Arg Glu Val Trp
 565 570 575

Lys Arg Leu His Asp Glu Gly Ile Ile Arg Leu Tyr Gln Arg Pro Gly
 580 585 590

Pro Gly Thr Ala Lys Ala Lys Asn
 595 600

<210> 30
 <211> 566
 <212> PRT
 <213> Gallus gallus

<220>
 <223> chicken alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I (ST6GalNAcTI)

<400> 30
 Met Gly Phe Leu Ile Arg Arg Leu Pro Lys Asp Ser Arg Ile Phe Arg
 1 5 10 15

Trp Leu Leu Ile Leu Thr Val Phe Ser Phe Ile Ile Thr Ser Phe Ser
 20 25 30

Ala Leu Phe Gly Met Glu Lys Ser Ile Phe Arg Gln Leu Lys Ile Tyr
 35 40 45

Gln Ser Ile Ala His Met Leu Gln Val Asp Thr Gln Asp Gln Gln Gly
 50 55 60

Ser Asn Tyr Ser Ala Asn Gly Arg Ile Ser Lys Val Gly Leu Glu Arg
 65 70 75 80

Asp Ile Ala Trp Leu Glu Leu Asn Thr Ala Val Ser Thr Pro Ser Gly
 85 90 95

Glu Gly Lys Glu Glu Gln Lys Lys Thr Val Lys Pro Val Ala Lys Val
 100 105 110

Glu Glu Ala Lys Glu Lys Val Thr Val Lys Pro Phe Pro Glu Val Met
 115 120 125

Gly Ile Thr Asn Thr Thr Ala Ser Thr Ala Ser Val Val Glu Arg Thr
 130 135 140

Lys Glu Lys Thr Thr Ala Arg Pro Val Pro Gly Val Gly Glu Ala Asp
 145 150 155 160

Gly Lys Arg Thr Thr Ile Ala Leu Pro Ser Met Lys Glu Asp Lys Glu
 165 170 175

Lys Ala Thr Val Lys Pro Ser Phe Gly Met Lys Val Ala His Ala Asn
 180 185 190

Ser Thr Ser Lys Asp Lys Pro Lys Ala Glu Glu Pro Pro Ala Ser Val
 195 200 205

Lys Ala Ile Arg Pro Val Thr Gln Ala Ala Thr Val Thr Glu Lys Lys
 210 215 220
 Lys Leu Arg Ala Ala Asp Phe Lys Thr Glu Pro Gln Trp Asp Phe Asp
 225 230 235 240
 Asp Glu Tyr Ile Leu Asp Ser Ser Ser Pro Val Ser Thr Cys Ser Glu
 245 250 255
 Ser Val Arg Ala Lys Ala Ala Lys Ser Asp Trp Leu Arg Asp Leu Phe
 260 265 270
 Leu Pro Asn Ile Thr Leu Phe Ile Asp Lys Ser Tyr Phe Asn Val Ser
 275 280 285
 Glu Trp Asp Arg Leu Glu His Phe Ala Pro Pro Tyr Gly Phe Met Glu
 290 295 300
 Leu Asn Tyr Ser Leu Val Glu Glu Val Met Ser Arg Leu Pro Pro Asn
 305 310 315 320
 Pro His Gln Gln Leu Leu Leu Ala Asn Ser Ser Ser Asn Val Ser Thr
 325 330 335
 Cys Ile Ser Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn Asn Ser
 340 345 350
 Gly Met Gly Gln Glu Ile Asp Ser His Asp Tyr Val Phe Arg Val Ser
 355 360 365
 Gly Ala Val Ile Lys Gly Tyr Glu Lys Asp Val Gly Thr Lys Thr Ser
 370 375 380
 Phe Tyr Gly Phe Thr Ala Tyr Ser Leu Val Ser Ser Leu Gln Asn Leu
 385 390 395 400
 Gly His Lys Gly Phe Lys Lys Ile Pro Gln Gly Lys His Ile Arg Tyr
 405 410 415
 Ile His Phe Leu Glu Ala Val Arg Asp Tyr Glu Trp Leu Lys Ala Leu
 420 425 430
 Leu Leu Asp Lys Asp Ile Arg Lys Gly Phe Leu Asn Tyr Tyr Gly Arg
 435 440 445
 Arg Pro Arg Glu Arg Phe Asp Glu Asp Phe Thr Met Asn Lys Tyr Leu
 450 455 460
 Val Ala His Pro Asp Phe Leu Arg Tyr Leu Lys Asn Arg Phe Leu Lys
 465 470 475 480
 Ser Lys Asn Leu Gln Lys Pro Tyr Trp Arg Leu Tyr Arg Pro Thr Thr
 485 490 495
 Gly Ala Leu Leu Leu Leu Thr Ala Leu His Leu Cys Asp Arg Val Ser
 500 505 510
 Ala Tyr Gly Tyr Ile Thr Glu Gly His Gln Lys Tyr Ser Asp His Tyr
 515 520 525

Tyr Asp Lys Glu Trp Lys Arg Leu Val Phe Tyr Val Asn His Asp Phe
 530 535 540
 Asn Leu Glu Lys Gln Val Trp Lys Arg Leu His Asp Glu Asn Ile Met
 545 550 555 560
 Lys Leu Tyr Gln Arg Ser
 565

<210> 31
 <211> 495
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mouse
 alpha-N-acetylgalactosaminide
 alpha-2,6-sialyltransferase I (ST6GalNACTI)
 beginning at residue 32 of the native mouse protein

<400> 31
 Asp Pro Arg Ala Lys Asp Ser Arg Cys Gln Phe Ile Trp Lys Asn Asp
 1 5 10 15
 Ala Ser Ala Gln Glu Asn Gln Gln Lys Ala Glu Pro Gln Val Pro Ile
 20 25 30
 Met Thr Leu Ser Pro Arg Val His Asn Lys Glu Ser Thr Ser Val Ser
 35 40 45
 Ser Lys Asp Leu Lys Lys Gln Glu Arg Glu Ala Val Gln Gly Glu Gln
 50 55 60
 Ala Glu Gly Lys Glu Lys Arg Lys Leu Glu Thr Ile Arg Pro Ala Pro
 65 70 75 80
 Glu Asn Pro Gln Ser Lys Ala Glu Pro Ala Ala Lys Thr Pro Val Ser
 85 90 95
 Glu His Leu Asp Lys Leu Pro Arg Thr Pro Gly Ala Leu Ser Thr Arg
 100 105 110
 Lys Thr Pro Met Ala Thr Gly Ala Val Pro Ala Lys Lys Val Val
 115 120 125
 Gln Ala Thr Lys Ser Pro Ala Ser Ser Pro His Pro Thr Thr Arg Arg
 130 135 140
 Arg Gln Arg Leu Lys Ala Ser Glu Phe Lys Ser Glu Pro Arg Trp Asp
 145 150 155 160
 Phe Glu Glu Glu Tyr Ser Leu Asp Met Ser Ser Leu Gln Thr Asn Cys
 165 170 175
 Ser Ala Ser Val Lys Ile Lys Ala Ser Lys Ser Pro Trp Leu Gln Asn
 180 185 190
 Ile Phe Leu Pro Asn Ile Thr Leu Phe Leu Asp Ser Gly Arg Phe Thr
 195 200 205

Gln Ser Glu Trp Asn Arg Leu Glu His Phe Ala Pro Pro Phe Gly Phe
 210 215 220
 Met Glu Leu Asn Gln Ser Leu Val Gln Lys Val Val Thr Arg Phe Pro
 225 230 235 240
 Pro Val Arg Gln Gln Leu Leu Leu Ala Ser Leu Pro Thr Gly Tyr
 245 250 255
 Ser Lys Cys Ile Thr Cys Ala Val Val Gly Asn Gly Gly Ile Leu Asn
 260 265 270
 Asp Ser Arg Val Gly Arg Glu Ile Asp Ser His Asp Tyr Val Phe Arg
 275 280 285
 Leu Ser Gly Ala Val Ile Lys Gly Tyr Glu Gln Asp Val Gly Thr Arg
 290 295 300
 Thr Ser Phe Tyr Gly Phe Thr Ala Phe Ser Leu Thr Gln Ser Ile Leu
 305 310 315 320
 Ile Leu Gly Arg Arg Gly Phe Gln His Val Pro Leu Gly Lys Asp Val
 325 330 335
 Arg Tyr Leu His Phe Leu Glu Gly Thr Arg Asn Tyr Glu Trp Leu Glu
 340 345 350
 Ala Met Phe Leu Asn Gln Thr Leu Ala Lys Thr His Leu Ser Trp Phe
 355 360 365
 Arg His Arg Pro Gln Glu Ala Phe Arg Asn Ala Leu Asp Leu Asp Arg
 370 375 380
 Tyr Leu Leu Leu His Pro Asp Phe Leu Arg Tyr Met Lys Asn Arg Phe
 385 390 395 400
 Leu Arg Ser Lys Thr Leu Asp Thr Ala His Trp Arg Ile Tyr Arg Pro
 405 410 415
 Thr Thr Gly Ala Leu Leu Leu Leu Thr Ala Leu His Leu Cys Asp Lys
 420 425 430
 Val Ser Ala Tyr Gly Phe Ile Thr Glu Gly His Gln Arg Phe Ser Asp
 435 440 445
 His Tyr Tyr Asp Thr Ser Trp Lys Arg Leu Ile Phe Tyr Ile Asn His
 450 455 460
 Asp Phe Arg Leu Glu Arg Met Val Trp Lys Arg Leu His Asp Glu Gly
 465 470 475 480
 Ile Ile Trp Leu Tyr Gln Arg Pro Gln Ser Asp Lys Ala Lys Asn
 485 490 495

<210> 32
 <211> 363
 <212> PRT
 <213> Homo sapiens

<220>

<223> full length human core 1
UDP-galactose:N-acetylgalactosamine-alpha-R
beta-1,3-galactosyltransferase (Core 1 Galt1)

<400> 32

Met Ala Ser Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Cys Gly Ser
1 5 10 15

Ala Ile Gly Phe Leu Leu Cys Ser Gln Leu Phe Ser Ile Leu Leu Gly
20 25 30

Glu Lys Val Asp Thr Gln Pro Asn Val Leu His Asn Asp Pro His Ala
35 40 45

Arg His Ser Asp Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn
50 55 60

Phe Asn Ala Asp Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala
65 70 75 80

Glu Asn Leu Tyr Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly
85 90 95

Pro Gln Asn Leu Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala
100 105 110

Gln Arg Cys Asn Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp
115 120 125

Phe Pro Ala Val Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr
130 135 140

Trp Lys Thr Ile Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Glu
145 150 155 160

Asp Ala Asp Trp Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu
165 170 175

Asp Asn Leu Arg Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile
180 185 190

Tyr Phe Gly Arg Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser
195 200 205

Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val
210 215 220

Asp Ala Phe Lys Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp
225 230 235 240

Leu Ala Leu Gly Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp
245 250 255

Ser Arg Asp Thr Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu
260 265 270

His His Leu Ile Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn
275 280 285

Tyr Asn Tyr Tyr Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu
290 295 300

Ala Val Ser Phe His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu
305 310 315 320

Tyr Leu Val Tyr His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln
325 330 335

Pro Thr Leu Pro Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys
340 345 350

Asn Glu Asp Thr Lys Val Lys Leu Gly Asn Pro
355 360

<210> 33

<211> 341

<212> PRT

<213> Drosophila melanogaster

<220>

<223> Drosophila core 1
UDP-galactose:N-acetylgalactosamine-alpha-R
beta-1,3-galactosyltransferase (Core 1 Galt1)

<400> 33

Glu Phe Met Pro Tyr Asp Gly His Arg His Gly Asp Val Asn Asp Ala
1 5 10 15

His His Ser His Asp Met Met Glu Met Ser Gly Pro Glu Gln Asp Val
20 25 30

Gly Gly His Glu His Val His Glu Asn Ser Thr Ile Ala Glu Arg Leu
35 40 45

Tyr Ser Glu Val Arg Val Leu Cys Trp Ile Met Thr Asn Pro Ser Asn
50 55 60

His Gln Lys Lys Ala Arg His Val Lys Arg Thr Trp Gly Lys Arg Cys
65 70 75 80

Asn Lys Leu Ile Phe Met Ser Ser Ala Lys Asp Asp Glu Leu Asp Ala
85 90 95

Val Ala Leu Pro Val Gly Glu Gly Arg Asn Asn Leu Trp Gly Lys Thr
100 105 110

Lys Glu Ala Tyr Lys Tyr Ile Tyr Glu His His Ile Asn Asp Ala Asp
115 120 125

Trp Phe Leu Lys Ala Asp Asp Asp Thr Tyr Thr Ile Val Glu Asn Met
130 135 140

Arg Tyr Met Leu Tyr Pro Tyr Ser Pro Glu Thr Pro Val Tyr Phe Gly
145 150 155 160

Cys Lys Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala
165 170 175

Gly Tyr Val Leu Ser Arg Glu Ala Val Arg Arg Phe Val Val Glu Ala
 180 185 190
 Leu Pro Asn Pro Lys Leu Cys Lys Ser Asp Asn Ser Gly Ala Glu Asp
 195 200 205
 Val Glu Ile Gly Lys Cys Leu Gln Asn Val Asn Val Leu Ala Gly Asp
 210 215 220
 Ser Arg Asp Ser Asn Gly Arg Gly Arg Phe Phe Pro Phe Val Pro Glu
 225 230 235 240
 His His Leu Ile Pro Ser His Thr Asp Lys Lys Phe Trp Tyr Trp Gln
 245 250 255
 Tyr Ile Phe Tyr Lys Thr Asp Glu Gly Leu Asp Cys Cys Ser Asp Asn
 260 265 270
 Ala Ile Ser Phe His Tyr Val Ser Pro Asn Gln Met Tyr Val Leu Asp
 275 280 285
 Tyr Leu Ile Tyr His Leu Arg Pro Tyr Gly Ile Ile Asn Thr Pro Asp
 290 295 300
 Ala Leu Pro Asn Lys Leu Ala Val Gly Glu Leu Met Pro Glu Ile Lys
 305 310 315 320
 Glu Gln Ala Thr Glu Ser Thr Ser Asp Gly Val Ser Lys Arg Ser Ala
 325 330 335
 Glu Thr Lys Thr Gln
 340

<210> 34
 <211> 341
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> Drosophila core 1
 UDP-galactose:N-acetylgalactosamine-alpha-R
 beta-1,3-galactosyltransferase (Core 1 Galt1)

<400> 34
 Glu Phe Met Pro Tyr Asp Gly His Arg His Gly Asp Val Asn Asp Ala
 1 5 10 15

His His Ser His Asp Met Met Glu Met Ser Gly Pro Glu Gln Asp Val
 20 25 30

Gly Gly His Glu His Val His Glu Asn Ser Thr Ile Ala Glu Arg Leu
 35 40 45

Tyr Ser Glu Val Arg Val Leu Cys Trp Ile Met Thr Asn Pro Ser Asn
 50 55 60

His Gln Lys Lys Ala Arg His Val Lys Arg Thr Trp Gly Lys Arg Cys
 65 70 75 80

Asn	Lys	Leu	Ile	Phe	Met	Ser	Ser	Ala	Lys	Asp	Asp	Glu	Leu	Asp	Ala
									85						95
Val	Ala	Leu	Pro	Val	Gly	Glu	Gly	Arg	Asn	Asn	Leu	Trp	Gly	Lys	Thr
									100		105			110	
Lys	Glu	Ala	Tyr	Lys	Tyr	Ile	Tyr	Glu	His	His	Ile	Asn	Asp	Ala	Asp
									115		120			125	
Trp	Phe	Leu	Lys	Ala	Asp	Asp	Asp	Thr	Tyr	Thr	Ile	Val	Glu	Asn	Met
									130		135			140	
Arg	Tyr	Met	Leu	Tyr	Pro	Tyr	Ser	Pro	Glu	Thr	Pro	Val	Tyr	Phe	Gly
									145		150			155	
Cys	Lys	Phe	Lys	Pro	Tyr	Val	Lys	Gln	Gly	Tyr	Met	Ser	Gly	Gly	Ala
									165		170			175	
Gly	Tyr	Val	Leu	Ser	Arg	Glu	Ala	Val	Arg	Arg	Phe	Val	Val	Glu	Ala
									180		185			190	
Leu	Pro	Asn	Pro	Lys	Leu	Cys	Lys	Ser	Asp	Asn	Ser	Gly	Ala	Glu	Asp
									195		200			205	
Val	Glu	Ile	Gly	Lys	Cys	Leu	Gln	Asn	Val	Asn	Val	Leu	Ala	Gly	Asp
									210		215			220	
Ser	Arg	Asp	Ser	Asn	Gly	Arg	Gly	Arg	Phe	Phe	Pro	Phe	Val	Pro	Glu
									225		230			235	
Ser	His	His	Leu	Ile	Pro	Ser	His	Thr	Asp	Lys	Lys	Phe	Trp	Tyr	Trp
									245		250			255	
Tyr	Ile	Phe	Tyr	Lys	Thr	Asp	Glu	Gly	Leu	Asp	Cys	Cys	Ser	Asp	Asn
									260		265			270	
Ala	Ile	Ser	Phe	His	Tyr	Val	Ser	Pro	Asn	Gln	Met	Tyr	Val	Leu	Asp
									275		280			285	
Tyr	Leu	Ile	Tyr	His	Leu	Arg	Pro	Tyr	Gly	Ile	Ile	Asn	Thr	Pro	Asp
									290		295			300	
Ala	Leu	Pro	Asn	Lys	Leu	Ala	Val	Gly	Glu	Leu	Met	Pro	Glu	Ile	Lys
									305		310			315	
Glu	Gln	Ala	Thr	Glu	Ser	Thr	Ser	Asp	Gly	Val	Ser	Lys	Arg	Ser	Thr
									325		330			335	
Glu	Thr	Lys	Thr	Gln											
									340						

<210> 35
<211> 371
<212> PRT
<213> *Yersinia pseudotuberculosis*

<220>
<223> maltose binding protein (MBP)

<400> 35

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

Gly Ile Lys Val Thr Ile Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Leu
65 70 75 80

Thr Pro Ser Lys Ala Phe Gln Glu Lys Leu Phe Pro Phe Thr Trp Asp
85 90 95

Ala Val Arg Phe Asn Gly Lys Leu Ile Gly Tyr Pro Val Ala Val Glu
100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Val Lys Glu Ala Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Thr Leu Arg Ala Asn Gly
130 135 140

Lys Ser Ala Ile Met Trp Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Val Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Phe Glu Asn Gly Val
165 170 175

Tyr Asp Ala Lys Asn Val Gly Val Asn Asn Ala Gly Ala Gln Ala Gly
180 185 190

Leu Gln Phe Ile Val Asp Leu Val Lys Asn Lys His Ile Asn Ala Asp
195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
210 215 220

Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Lys Ser Lys
225 230 235 240

Ile Asn Tyr Gly Val Thr Leu Leu Pro Thr Phe His Gly Gln Pro Ser
245 250 255

Lys Pro Phe Val Gly Val Leu Thr Ala Gly Ile Asn Ala Ala Ser Pro
260 265 270

Asn Lys Glu Leu Ala Thr Glu Phe Leu Glu Asn Tyr Leu Ile Thr Asp
275 280 285

Gln Gly Leu Ala Glu Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
290 295 300

Leu Lys Ser Phe Gln Glu Gln Leu Ala Lys Asp Pro Arg Ile Ala Ala
305 310 315 320

Thr Met Asp Asn Ala Thr Asn Gly Glu Ile Met Pro Asn Ile Pro Gln
325 330 335

Met Ala Ala Phe Trp Tyr Ala Thr Arg Ser Ala Val Leu Asn Ala Ile
340 345 350

Thr Gly Arg Gln Thr Val Glu Ala Ala Leu Asn Asp Ala Ala Thr Arg
355 360 365

Ile Thr Lys
370

<210> 36

<211> 369

<212> PRT

<213> Escherichia coli

<220>

<223> maltose binding protein (MBP)

<400> 36

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
85 90 95

Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
180 185 190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365

Ser

<210> 37
 <211> 381
 <212> PRT
 <213> Pyrococcus furiosus

 <220>
 <223> maltose binding protein (MBP)

 <400> 37
 Met Lys Ile Glu Glu Gly Lys Val Val Ile Trp His Ala Met Gln Pro
 1 5 10 15
 Asn Glu Leu Glu Val Phe Gln Ser Leu Ala Glu Glu Tyr Met Ala Leu
 20 25 30
 Ser Pro Glu Val Glu Ile Val Phe Glu Gln Lys Pro Asn Leu Glu Asp
 35 40 45
 Ala Leu Lys Ala Ala Ile Pro Thr Gly Gln Gly Pro Asp Leu Phe Ile
 50 55 60
 Trp Ala His Asp Trp Ile Gly Lys Phe Ala Glu Ala Gly Leu Leu Glu
 65 70 75 80
 Pro Ile Asp Glu Tyr Val Thr Glu Asp Leu Leu Asn Glu Phe Ala Pro
 85 90 95

Met Ala Gln Asp Ala Met Gln Tyr Lys Gly His Tyr Tyr Ala Leu Pro
 100 105 110
 Phe Ala Ala Glu Thr Val Ala Ile Ile Tyr Asn Lys Glu Met Val Ser
 115 120 125
 Glu Pro Pro Lys Thr Phe Asp Glu Met Lys Ala Ile Met Glu Lys Tyr
 130 135 140
 Tyr Asp Pro Ala Asn Glu Lys Tyr Gly Ile Ala Trp Pro Ile Asn Ala
 145 150 155 160
 Tyr Phe Ile Ser Ala Ile Ala Gln Ala Phe Gly Gly Tyr Tyr Phe Asp
 165 170 175
 Asp Lys Thr Glu Gln Pro Gly Leu Asp Lys Pro Glu Thr Ile Glu Gly
 180 185 190
 Phe Lys Phe Phe Thr Glu Ile Trp Pro Tyr Met Ala Pro Thr Gly
 195 200 205
 Asp Tyr Asn Thr Gln Gln Ser Ile Phe Leu Glu Gly Arg Ala Pro Met
 210 215 220
 Met Val Asn Gly Pro Trp Ser Ile Asn Asp Val Lys Lys Ala Gly Ile
 225 230 235 240
 Asn Phe Gly Val Val Pro Leu Pro Pro Ile Ile Lys Asp Gly Lys Glu
 245 250 255
 Tyr Trp Pro Arg Pro Tyr Gly Val Lys Leu Ile Tyr Phe Ala Ala
 260 265 270
 Gly Ile Lys Asn Lys Asp Ala Ala Trp Lys Phe Ala Lys Trp Leu Thr
 275 280 285
 Thr Ser Glu Glu Ser Ile Lys Thr Leu Ala Leu Glu Leu Gly Tyr Ile
 290 295 300
 Pro Val Leu Thr Lys Val Leu Asp Asp Pro Glu Ile Lys Asn Asp Pro
 305 310 315 320
 Val Ile Tyr Gly Phe Gly Gln Ala Val Gln His Ala Tyr Leu Met Pro
 325 330 335
 Lys Ser Pro Lys Met Ser Ala Val Trp Gly Gly Val Asp Gly Ala Ile
 340 345 350
 Asn Glu Ile Leu Gln Asp Pro Gln Asn Ala Asp Ile Glu Gly Ile Leu
 355 360 365
 Lys Lys Tyr Gln Gln Glu Ile Leu Asn Asn Met Gln Gly
 370 375 380

<210> 38
 <211> 412
 <212> PRT
 <213> Thermococcus litoralis

<220>

<223> maltose binding protein (MBP)

<400> 38

Met Lys Ile Glu Glu Gly Lys Ile Val Phe Ala Val Gly Gly Ala Pro
1 5 10 15

Asn Glu Ile Glu Tyr Trp Lys Gly Val Ile Ala Glu Phe Glu Lys Lys
20 25 30

Tyr Pro Gly Val Thr Val Glu Leu Lys Arg Gln Ala Thr Asp Thr Glu
35 40 45

Gln Arg Arg Leu Asp Leu Val Asn Ala Leu Arg Gly Lys Ser Ser Asp
50 55 60

Pro Asp Val Phe Leu Met Asp Val Ala Trp Leu Gly Gln Phe Ile Ala
65 70 75 80

Ser Gly Trp Leu Glu Pro Leu Asp Asp Tyr Val Gln Lys Asp Asn Tyr
85 90 95

Asp Leu Ser Val Phe Phe Gln Ser Val Ile Asn Leu Ala Asp Lys Gln
100 105 110

Gly Gly Lys Leu Tyr Ala Leu Pro Val Tyr Ile Asp Ala Gly Leu Leu
115 120 125

Tyr Tyr Arg Lys Asp Leu Leu Glu Lys Tyr Gly Tyr Ser Lys Pro Pro
130 135 140

Glu Thr Trp Gln Glu Leu Val Glu Met Ala Gln Lys Ile Gln Ser Gly
145 150 155 160

Glu Arg Glu Thr Asn Pro Asn Phe Trp Gly Phe Val Trp Gln Gly Lys
165 170 175

Gln Tyr Glu Gly Leu Val Cys Asp Phe Val Glu Tyr Val Tyr Ser Asn
180 185 190

Gly Gly Ser Leu Gly Glu Phe Lys Asp Gly Lys Trp Val Pro Thr Leu
195 200 205

Asn Lys Pro Glu Asn Val Glu Ala Leu Gln Phe Met Val Asp Leu Ile
210 215 220

His Lys Tyr Lys Ile Ser Pro Pro Asn Thr Tyr Thr Glu Met Thr Glu
225 230 235 240

Glu Pro Val Arg Leu Met Phe Gln Gln Gly Asn Ala Ala Phe Glu Arg
245 250 255

Asn Trp Pro Tyr Ala Trp Gly Leu His Asn Ala Asp Asp Ser Pro Val
260 265 270

Lys Gly Lys Val Gly Val Ala Pro Leu Pro His Phe Pro Gly His Lys
275 280 285

Ser Ala Ala Thr Leu Gly Gly Trp His Ile Gly Ile Ser Lys Tyr Ser
290 295 300

Asp	Asn	Lys	Ala	Leu	Ala	Trp	Glu	Phe	Val	Lys	Phe	Val	Glu	Ser	Tyr
305															320
Ser	Val	Gln	Lys	Gly	Phe	Ala	Met	Asn	Leu	Gly	Trp	Asn	Pro	Gly	Arg
				325					330						335
Val	Asp	Val	Tyr	Asp	Asp	Pro	Ala	Val	Val	Ser	Ser	Pro	His	Leu	
								340	345						350
Lys	Glu	Leu	Arg	Ala	Val	Phe	Glu	Asn	Ala	Val	Pro	Arg	Pro	Ile	Val
								355	360						365
Pro	Tyr	Tyr	Pro	Gln	Leu	Ser	Glu	Ile	Ile	Gln	Lys	Tyr	Val	Asn	Ser
								370	375						380
Ala	Leu	Ala	Gly	Lys	Ile	Ser	Pro	Gln	Glu	Ala	Leu	Asp	Lys	Ala	Gln
								385	390						400
Lys	Glu	Ala	Glu	Glu	Leu	Val	Lys	Gln	Tyr	Ser	Lys				
								405	410						

<210> 39
 <211> 378
 <212> PRT
 <213> Thermatoga maritime

<220>
 <223> maltose binding protein (MBP)

<400> 39															
Met	Lys	Ile	Glu	Gln	Thr	Lys	Leu	Thr	Ile	Trp	Ser	Ser	Glu	Lys	Gln
1					5				10						15
Val	Asp	Ile	Leu	Gln	Lys	Leu	Gly	Glu	Glu	Phe	Lys	Ala	Lys	Tyr	Gly
								20	25						30
Ile	Pro	Val	Glu	Val	Gln	Tyr	Val	Asp	Phe	Gly	Ser	Ile	Lys	Ser	Lys
								35	40						45
Phe	Leu	Thr	Ala	Ala	Pro	Gln	Gly	Gln	Gly	Ala	Asp	Ile	Ile	Val	Gly
								50	55						60
Ala	His	Asp	Trp	Val	Gly	Glu	Leu	Ala	Val	Asn	Gly	Leu	Ile	Glu	Pro
								65	70						80
Ile	Pro	Asn	Phe	Ser	Asp	Leu	Lys	Asn	Phe	Tyr	Asp	Thr	Ala	Leu	Lys
								85	90						95
Ala	Phe	Ser	Tyr	Gly	Gly	Lys	Leu	Tyr	Gly	Val	Pro	Tyr	Ala	Met	Glu
								100	105						110
Ala	Val	Ala	Leu	Ile	Tyr	Asn	Lys	Asp	Tyr	Val	Asp	Ser	Val	Pro	Lys
								115	120						125
Thr	Met	Asp	Glu	Leu	Ile	Glu	Lys	Ala	Lys	Gln	Ile	Asp	Glu	Glu	Tyr
								130	135						140
Gly	Gly	Glu	Val	Arg	Gly	Phe	Ile	Tyr	Asp	Val	Ala	Asn	Phe	Tyr	Phe
								145	150						160

Ser Ala Pro Phe Ile Leu Gly Tyr Gly Gly Tyr Val Phe Lys Glu Thr
 165 170 175
 Pro Gln Gly Leu Asp Val Thr Asp Ile Gly Leu Ala Asn Glu Gly Ala
 180 185 190
 Val Lys Gly Ala Lys Leu Ile Lys Arg Met Ile Asp Glu Gly Val Leu
 195 200 205
 Thr Pro Gly Asp Asn Tyr Gly Thr Met Asp Ser Met Phe Lys Glu Gly
 210 215 220
 Leu Ala Ala Met Ile Ile Asn Gly Leu Trp Ala Ile Lys Ser Tyr Lys
 225 230 235 240
 Asp Ala Gly Ile Asn Tyr Gly Val Ala Pro Ile Pro Glu Leu Glu Pro
 245 250 255
 Gly Val Pro Ala Lys Pro Phe Val Gly Val Gln Gly Phe Met Ile Asn
 260 265 270
 Ala Lys Ser Pro Asn Lys Val Ile Ala Met Glu Phe Leu Thr Asn Phe
 275 280 285
 Ile Ala Arg Lys Glu Thr Met Tyr Lys Ile Tyr Leu Ala Asp Pro Arg
 290 295 300
 Leu Pro Ala Arg Lys Asp Val Leu Glu Leu Val Lys Asp Asn Pro Asp
 305 310 315 320
 Val Val Ala Phe Thr Gln Ser Ala Ser Met Gly Thr Pro Met Pro Asn
 325 330 335
 Val Pro Glu Met Ala Pro Val Trp Ser Ala Met Gly Asp Ala Leu Ser
 340 345 350
 Ile Ile Ile Asn Gly Gln Ala Ser Val Glu Asp Ala Leu Lys Glu Ala
 355 360 365
 Val Asp Lys Ile Lys Ala Gln Ile Glu Lys
 370 375

<210> 40
 <211> 372
 <212> PRT
 <213> Vibrio cholerae

<220>
 <223> maltose binding protein (MBP)

<400> 40
 Met Lys Ile Glu Glu Gly Gln Leu Thr Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Ala Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Ala His Pro Asp Ala Leu Gln Asp Lys Phe
 35 40 45

Pro Gln Thr Ala Ala Thr Gly Asp Gly Pro Asp Ile Val Phe Trp Ala
 50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Glu Ala Gly Leu Leu Val Glu Ile
 65 70 75 80

Lys Pro Ser Ala Lys Ile Gln Glu Gly Ile Val Asp Phe Ala Trp Asp
 85 90 95

Ala Val Lys Tyr Asn Gly Lys Ile Ile Gly Tyr Pro Ile Ala Val Glu
 100 105 110

Ser Leu Ser Leu Ile Tyr Asn Lys Asp Leu Val Pro Asn Pro Pro Lys
 115 120 125

Ser Trp Glu Glu Val Ala Glu Leu Asp Ala Lys Leu Lys Lys Glu Gly
 130 135 140

Lys Ser Ala Ile Met Trp Asn Leu Lys Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160

Leu Met Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Gly Val Asp Gly
 165 170 175

Tyr Asp Val Lys Asp Ala Gly Ile Asn Asn Lys Gly Val Lys Asp Ala
 180 185 190

Met Asn Phe Val Lys Gly Leu Val Asp Lys Gly Val Ile Ser Pro Asp
 195 200 205

Met Asp Tyr Ser Val Ser Glu Ser Ala Phe Asn Gln Gly Asn Thr Ala
 210 215 220

Met Thr Ile Asn Gly Pro Trp Ser Trp Gly Asn Ile Glu Lys Ser Gly
 225 230 235 240

Ile Asn Tyr Gly Val Thr Thr Leu Pro Lys Phe Asn Gly Gln Ala Ser
 245 250 255

Lys Pro Phe Val Gly Val Leu Thr Ala Gly Ile Ser Thr Ala Ser Pro
 260 265 270

Asn Lys Asp Leu Ala Val Glu Phe Ile Glu Asn Tyr Leu Leu Thr Asn
 275 280 285

Asp Gly Leu Arg Met Val Asn Asn Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300

Leu Asn Ser Phe Gln Arg Glu Leu Asp Ala Asp Ala Arg Ile Ala Ala
 305 310 315 320

Thr Met Asp Asn Ala Met Asn Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335

Met Asn Ala Phe Trp Ser Ser Ala Lys Asn Ala Ile Ile Asn Ile Val
 340 345 350

Asp Gly Arg Gln Thr Val Asp Ala Ala Leu Ala Asp Ala Glu Lys Gln
 355 360 365
 Met Thr Lys Pro
 370

<210> 41
 <211> 559
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human UDP-N-acetylgalactosaminyltransferase 1
 (GalNAcT1)

<400> 41
 Met Arg Lys Phe Ala Tyr Cys Lys Val Val Leu Ala Thr Ser Leu Ile
 1 5 10 15

Trp Val Leu Leu Asp Met Phe Leu Leu Tyr Phe Ser Glu Cys Asn
 20 25 30

Lys Cys Asp Glu Lys Lys Glu Arg Gly Leu Pro Ala Gly Asp Val Leu
 35 40 45

Glu Pro Val Gln Lys Pro His Glu Gly Pro Gly Glu Met Gly Lys Pro
 50 55 60

Val Val Ile Pro Lys Glu Asp Gln Glu Lys Met Lys Glu Met Phe Lys
 65 70 75 80

Ile Asn Gln Phe Asn Leu Met Ala Ser Glu Met Ile Ala Leu Asn Arg
 85 90 95

Ser Leu Pro Asp Val Arg Leu Glu Gly Cys Lys Thr Lys Val Tyr Pro
 100 105 110

Asp Asn Leu Pro Thr Thr Ser Val Val Ile Val Phe His Asn Glu Ala
 115 120 125

Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Ile Asn Arg Ser Pro
 130 135 140

Arg His Met Ile Glu Glu Ile Val Leu Val Asp Asp Ala Ser Glu Arg
 145 150 155 160

Asp Phe Leu Lys Arg Pro Leu Glu Ser Tyr Val Lys Lys Leu Lys Val
 165 170 175

Pro Val His Val Ile Arg Met Glu Gln Arg Ser Gly Leu Ile Arg Ala
 180 185 190

Arg Leu Lys Gly Ala Ala Val Ser Lys Gly Gln Val Ile Thr Phe Leu
 195 200 205

Asp Ala His Cys Glu Cys Thr Val Gly Trp Leu Glu Pro Leu Leu Ala
 210 215 220

Arg Ile Lys His Asp Arg Arg Thr Val Val Cys Pro Ile Ile Asp Val
 225 230 235 240

Ile Ser Asp Asp Thr Phe Glu Tyr Met Ala Gly Ser Asp Met Thr Tyr
 245 250 255
 Gly Gly Phe Asn Trp Lys Leu Asn Phe Arg Trp Tyr Pro Val Pro Gln
 260 265 270
 Arg Glu Met Asp Arg Arg Lys Gly Asp Arg Thr Leu Pro Val Arg Thr
 275 280 285
 Pro Thr Met Ala Gly Gly Leu Phe Ser Ile Asp Arg Asp Tyr Phe Gln
 290 295 300
 Glu Ile Gly Thr Tyr Asp Ala Gly Met Asp Ile Trp Gly Gly Glu Asn
 305 310 315 320
 Leu Glu Ile Ser Phe Arg Ile Trp Gln Cys Gly Gly Thr Leu Glu Ile
 325 330 335
 Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala Thr Pro Tyr
 340 345 350
 Thr Phe Pro Gly Gly Thr Gly Gln Ile Ile Asn Lys Asn Asn Arg Arg
 355 360 365
 Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr Ile Ile
 370 375 380
 Ser Pro Gly Val Thr Lys Val Asp Tyr Gly Asp Ile Ser Ser Arg Val
 385 390 395 400
 Gly Leu Arg His Lys Leu Gln Cys Lys Pro Phe Ser Trp Tyr Leu Glu
 405 410 415
 Asn Ile Tyr Pro Asp Ser Gln Ile Pro Arg His Tyr Phe Ser Leu Gly
 420 425 430
 Glu Ile Arg Asn Val Glu Thr Asn Gln Cys Leu Asp Asn Met Ala Arg
 435 440 445
 Lys Glu Asn Glu Lys Val Gly Ile Phe Asn Cys His Gly Met Gly Gly
 450 455 460
 Asn Gln Val Phe Ser Tyr Thr Ala Asn Lys Glu Ile Arg Thr Asp Asp
 465 470 475 480
 Leu Cys Leu Asp Val Ser Lys Leu Asn Gly Pro Val Thr Met Leu Lys
 485 490 495
 Cys His His Leu Lys Gly Asn Gln Leu Trp Glu Tyr Asp Pro Val Lys
 500 505 510
 Leu Thr Leu Gln His Val Asn Ser Asn Gln Cys Leu Asp Lys Ala Thr
 515 520 525
 Glu Glu Asp Ser Gln Val Pro Ser Ile Arg Asp Cys Asn Gly Ser Arg
 530 535 540
 Ser Gln Gln Trp Leu Leu Arg Asn Val Thr Leu Pro Glu Ile Phe
 545 550 555

<210> 42
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 42
Lys Met Leu Leu
1

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 43
Ile Trp Val Leu
1

<210> 44
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 44
Arg Ala Ile Pro Asp
1 5

<210> 45
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 45
Thr Ser Val Val Ile
1 5

<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 46
Phe His Asn Glu Ala
1 5

<210> 47
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 47
Leu Leu Arg Thr Val
1 5

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 48
Glu Ile Ile Leu Val Asp Asp
1 5

<210> 49
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 49
Gly Leu Ile Arg Ala Arg Leu Lys Gly Ala
1 5 10

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 50
Val Ile Thr Phe Leu Asp Ala His Cys Glu Cys
1 5 10

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 51
Trp Leu Glu Pro Leu Leu
1 5

<210> 52
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 52
Pro Ile Ile Asp Val Ile
1 5

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 53
Tyr Met Ala Ala Ser
1 5

<210> 54
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 54
Pro Ile Lys Thr Pro
1 5

> >

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 55
Ile Ala Gly Gly Leu Phe
1 5

<210> 56
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 56
Met Asp Ile Trp Gly Gly Glu Asn Leu Glu Ile Ser Phe Arg Ile Trp
1 5 10 15

Gln Cys Gly Gly Ser Leu Glu Ile Ile
20 25

<210> 57
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 57
Val Gly His Val Phe Arg Lys
1 5

<210> 58
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 58
Pro Tyr Thr Phe Pro Gly Gly Ser Gly
1 5

<210> 59
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 59
Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr
1 5 10

<210> 60
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 60
Cys Lys Pro Phe
1

<210> 61
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 61
Trp Tyr Leu Glu Asn Ile Tyr Pro Asp
1 5

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus peptide

<400> 62
Val Gly Ile Phe
1

<210> 63
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 63
Gly Gly Asn Gln
1

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 64
Asp Leu Cys Leu
1

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:consensus
peptide

<400> 65
Ser Gln Gln Trp
1

<210> 66
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-FLAG
antibody epitope tag, "FLAG tag"

<400> 66
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:hexahistidine
affinity tag, polyhistidine purification tag, poly
His, metal chelate affinity ligand

```

<400> 67
His His His His His His
1 5

<210> 68
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
      amplification sense primer Sial 5' Tm

<400> 68
tttggatcca agctacactt actccaatgg 30

<210> 69
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
      amplification antisense primer Sial 3' Whole

<400> 69
tttgaattct cagataccac tgcttaagtc 30

<210> 70
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
      amplification sense primer ST3BAMH1

<400> 70
taatggattc aagctacact tactccaaatg g 31

<210> 71
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
      amplification antisense primer ST3XBA1

<400> 71
gcgcgtctaga tcagataccca ctgcttaagt 30

<210> 72
<211> 35
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:PCR 5' primer
      ST3 BamH1 delta73

<400> 72
tgtatcgat ccctggccac caagtacgct aactt 35

<210> 73
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR 5' primer
      ST3 BamH1 delta85

<400> 73
tgtatcgat cctgcaaacc cggctacgct tcagccat 38

<210> 74
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR 5' primer
      ST3 BamH1 delta86

<400> 74
tgtatcgat ccaaaccgg ctacgcttca gccat 35

<210> 75
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR common 3'
      primer ST3-Xhol

<400> 75
ggtctcctcg agtcagatac cactgcttaa 30

<210> 76
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic
      oligonucleotide GnT1 R120A C121H+

<400> 76
ccgcagcact gttcggggccc acctggacaa gctgctg 37

```

```

<210> 77
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic
      oligonucleotide GnT1 R120A C121H-

<400> 77
cagcagcttg tccaggtggg cccgaacagt gctgcgg 37

<210> 78
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic
      oligonucleotide GnT1C123A+

<400> 78
agcactgttc ggcgccct ggacaagctg ctg 33

<210> 79
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic
      oligonucleotide GnT1C123A-

<400> 79
cagcagcttg tccagggcgc gccgaacagt gct 33

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MuC-2-like
      GalNAc peptide acceptor

<400> 80
Met Val Thr Pro Thr Pro Thr Pro Thr Cys
    1           5           10

```